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OM protein - protein search, using sw model

Run on: July 7, 2004, 05:56:13 ; Search time 34.232 Seconds

(without alignments)
637.949 Million cell updates/sec

Title: US-10-622-237-4

Perfect score: 2197

Sequence: 1 AAPPGLRLRLLLLSAAL.....TALINAGGONNSEEKKEVF 423

Scoring table:

BLOSUM62

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PTUS.COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2197	100.0	423	US-09-778-510-22	Sequence 22, App1
2	2169	98.7	442	US-09-778-510-20	Sequence 20, App1
3	2169	98.7	442	US-09-930-803-1	Sequence 1, App1
4	2149	97.8	440	US-09-866-028-61	Sequence 61, App1
5	904	41.1	444	US-08-653-984A-5	Sequence 5, App1
6	904	41.1	444	US-08-660-531-5	Sequence 5, App1
7	893.5	40.7	421	US-08-658-984A-1	Sequence 1, App1
8	893.5	40.7	421	US-08-660-531-1	Sequence 1, App1
9	738.5	33.6	398	US-09-778-510-6	Sequence 6, App1
10	732.5	33.3	398	US-09-778-510-6	Sequence 6, App1
11	732.5	33.3	398	US-09-907-794A-84	Sequence 84, App1
12	732.5	33.3	398	US-09-905-125A-84	Sequence 84, App1
13	732.5	33.3	398	US-09-903-775A-84	Sequence 84, App1
14	715.5	33.6	432	US-09-778-510-2	Sequence 2, App1
15	333	15.2	227	US-09-205-258-47	Sequence 47, App1
16	252.5	11.5	517	US-09-723-368-4	Sequence 4, App1
17	244	11.1	518	US-09-919-112-20	Sequence 20, App1
18	231.5	10.5	393	US-08-429-742-2	Sequence 2, App1
19	226.5	10.3	479	US-09-723-368-2	Sequence 2, App1
20	220.5	10.0	458	US-09-700-397-3	Sequence 3, App1
21	216	9.8	458	US-09-435-956A-1	Sequence 1, App1
22	212	9.6	308	US-09-700-397-4	Sequence 4, App1
23	206.5	9.4	308	US-08-414-657D-46	Sequence 46, App1
24	206.5	9.4	325	US-08-414-657D-2	Sequence 2, App1
25	206.5	9.4	325	US-08-414-657D-41	Sequence 41, App1
26	206.5	9.4	325	US-09-135-080-2	Sequence 2, App1
27	206.5	9.4	338	US-09-976-594-404	Sequence 404, App1

28	206	9.4	388	1	US-08-429-742-4	Sequence 4, App1
29	205.5	9.4	582	4	US-09-702-705-334	Sequence 334, App
30	205.5	9.4	582	4	US-09-736-457-334	Sequence 334, App
31	205.5	9.4	582	4	US-09-614-124B-334	Sequence 334, App
32	205.5	9.4	582	4	US-09-671-325-334	Sequence 334, App
33	205.5	9.4	582	4	US-09-589-184-334	Sequence 334, App
34	204.5	9.3	315	2	US-08-414-657D-47	Sequence 47, App1
35	204.5	9.3	338	2	US-08-414-657D-42	Sequence 42, App1
36	204.5	9.3	338	2	US-08-414-657D-43	Sequence 43, App1
37	204.5	9.3	338	4	US-09-135-080-4	Sequence 4, App1
38	204	9.3	642	1	US-08-217-299-1	Sequence 1, App1
39	204	9.3	698	2	US-08-602-725-36	Sequence 36, App1
40	204	9.3	734	2	US-08-389-459A-17	Sequence 17, App1
41	204	9.3	734	2	US-08-387-867B-17	Sequence 17, App1
42	203.5	9.3	583	3	US-08-432-016-2	Sequence 2, App1
43	203.5	9.3	583	2	US-08-684-594-2	Sequence 2, App1
44	203	9.2	1461	4	US-09-976-594-531	Sequence 531, App
45	198.5	9.0	338	2	US-08-414-657D-60	Sequence 60, App1

ALIGNMENTS

RESULT 1
US-09-778-510-22
Sequence 22, Application US/09778510
Patent No. 6512095
GENERAL INFORMATION:
APPLICANT: Baum, Peter
TITLE OF INVENTION: Molecules Designated B7L1
FILE REFERENCE: 2844-US
CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: PCT/US99/17906
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: 60/095,663
PRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 22
LENGTH: 423
TYPE: PRT
ORGANISM: Mus musculus
US-09-778-510-22

Query Match	100.0%;	Score 2197;	DB 4;	Length 423;
Best Local Similarity	100.0%;	Pred. No. 3,6e-187;		
Matches 423;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	AAPPGRLRLLLLLLSAALLPTGDGQNLFTKQVYIEGEVATISGVNKS	1	DSVTQLN 60
Dp	1	AAPPGRLRLLLLLLSAALLPTGGQQLFTKQVYIEGEVATISGVNKS	1	DSVTQLN 60
Qy	61	PNRQTIIFRDFRPLKDSRFQNLNFSSELKVSITNVSISDEGRYF	61	COLYTPDQESYTTI 120
Dp	61	PNRQTIIFRDFRPLKDSRFQNLNFSSELKVSITNVSISDEGRYF	61	COLYTPDQESYTTI 120
Qy	121	TVLPPRNLMIDIOKDTAVEGEIEVNCTPMASKPATITIRMFNGKELGKS	121	VEEWSM 180
Dp	121	TVLPPRNLMIDIOKDTAVEGEIEVNCTPMASKPATITIRMFNGKELGKS	121	VEEWSM 180
Qy	181	YTTTSQMLKKKKEDDGPVYICQEHFAYTGNLQIQRYIEVQYKPOVH	181	QMTYPIQGLR 240
Dp	181	YTTTSQMLKKKKEDDGPVYICQEHFAYTGNLQIQRYIEVQYKPOVH	181	QMTYPIQGLR 240
Qy	241	EGDAFEITCEAIGKQPMVTVVRVDDEMFOHAVLSGPNLFINNKUN	241	GTNGYRCEASNI 300
Dp	241	EGDAFEITCEAIGKQPMVTVVRVDDEMFOHAVLSGPNLFINNKUN	241	GTNGYRCEASNI 300
Qy	301	VGKAHSDVMYVVDPPTTTTTTTTTTTTTTTTTTTTTTTTTSRAAE	301	EECTGADVAVTG 360
Dp	301	VGKAHSDVMYVVDPPTTTTTTTTTTTTTTTTTTTTTTTTITDSRA	301	EEBEGIGADVAVTG 360

QY 361 GVAVVVFAMLCIIILIGRYFARHKGTYFTHKAGADDAADDAADTAIINAEAGGONNSEKK 420
DB 361 GVAVVVFAMLCIIILIGRYFARHKGTYFTHKAGADDAADDAADTAIINAEAGGONNSEKK 420
QY 421 EYF 423
DB 421 EYF 423

RESULT 2

US-09-778-510-20
Sequence 20, Application US/09778510
Patent No. 6512095
GENERAL INFORMATION:
APPLICANT: Baum, Peter
TITLE OF INVENTION: Molecules Designated B7L1
FILE REFERENCE: 2844-US
CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: PCT/US99/17906
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: 60/095,663
PRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 20
LENGTH: 442
TYPE: PRT
ORGANISM: Homo sapiens
US-09-778-510-20

Query Match 98.7%; Score 2169; DB 4; Length 442;
Best Local Similarity 98.8%; Pred. No. 1,2e-184;
Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPPGLRLRLILLLLSAALIPFGDQNLFTKQVTVIEGEVATISQVNSKSDSVIQLLN 60
DB 19 AAPPGLRLRLILLLLSAALIPFGDQNLFTKQVTVIEGEVATISQVNSKSDSVIQLLN 78
QY 61 PNRQTIYFRDPRFKDSRFQNLNFSSELKVSILTVNSISDEGRYFCQLYTDPPQESYTTI 120
DB 79 PNRQTIYFRDPRFKDSRFQNLNFSSELKVSILTVNSISDEGRYFCQLYTDPPQESYTTI 138
QY 121 TVVPPRNLMIDIOKDTAVAGEEIEVNCTAMASKPATIRFKNGKTELKSGSEVEEWSMD 180
DB 139 TVVPPRNLMIDIOKDTAVAGEEIEVNCTAMASKPATIRFKNGKTELKSGSEVEEWSMD 198
QY 181 YTVTSQMLKVKHEDDGVVICQVEHPAVTGNLTQRYLEYQYKQVHIQMTYPLQGLTR 240
DB 199 YTVTSQMLKVKHEDDGVVICQVEHPAVTGNLTQRYLEYQYKQVHIQMTYPLQGLTR 258
QY 241 EGDAPFELTCEAIGKQCPVMTWVRVDDEMPQHAIVSGNLFNNLNKTDNGTYRCEASNI 300
DB 259 EGDAPFELTCEAIGKQCPVMTWVRVDDEMPQHAIVSGNLFNNLNKTDNGTYRCEASNI 318
QY 301 VGKASDYMLYVDDPTTIPPTTTTTTTTTTTTTTTTTTTTTITDSRAGEGSIKAVDHAIVG 360
DB 319 VGKASDYMLYVDDPTTIPPTTTTTTTTTTTTTTTTTTTTTITDSRAGEGSIKAVDHAIVG 378
QY 361 GVAVVVFAMLCIIILIGRYFARHKGTYFTHKAGADDAADDAADTAIINAEAGGONNSEKK 420
DB 379 GVAVVVFAMLCIIILIGRYFARHKGTYFTHKAGADDAADDAADTAIINAEAGGONNSEKK 438
QY 421 EYF 423
DB 439 EYF 441

RESULT 3

US-09-930-803-1
Sequence 1, Application US/09930803
Patent No. 6596493
GENERAL INFORMATION:

APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: REEVES, Roger
APPLICANT: YOSHINOBI, Mutsaers
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS
FILE REFERENCE: JHU1770-1
CURRENT APPLICATION NUMBER: US/09/930,803
CURRENT FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 442
TYPE: PRT
ORGANISM: Homo sapiens
US-09-930-803-1

Query Match 98.7%; Score 2169; DB 4; Length 442;
Best Local Similarity 98.8%; Pred. No. 1,2e-184;
Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPPGLRLRLILLLLSAALIPFGDQNLFTKQVTVIEGEVATISQVNSKSDSVIQLLN 60
DB 19 AAPPGLRLRLILLLLSAALIPFGDQNLFTKQVTVIEGEVATISQVNSKSDSVIQLLN 78
QY 61 PNRQTIYFRDPRFKDSRFQNLNFSSELKVSILTVNSISDEGRYFCQLYTDPPQESYTTI 120
DB 79 PNRQTIYFRDPRFKDSRFQNLNFSSELKVSILTVNSISDEGRYFCQLYTDPPQESYTTI 138
QY 121 TVVPPRNLMIDIOKDTAVAGEEIEVNCTAMASKPATIRFKNGKTELKSGSEVEEWSMD 180
DB 139 TVVPPRNLMIDIOKDTAVAGEEIEVNCTAMASKPATIRFKNGKTELKSGSEVEEWSMD 198
QY 181 YTVTSQMLKVKHEDDGVVICQVEHPAVTGNLTQRYLEYQYKQVHIQMTYPLQGLTR 240
DB 199 YTVTSQMLKVKHEDDGVVICQVEHPAVTGNLTQRYLEYQYKQVHIQMTYPLQGLTR 258
QY 241 EGDAPFELTCEAIGKQCPVMTWVRVDDEMPQHAIVSGNLFNNLNKTDNGTYRCEASNI 300
DB 259 EGDAPFELTCEAIGKQCPVMTWVRVDDEMPQHAIVSGNLFNNLNKTDNGTYRCEASNI 318
QY 301 VGKASDYMLYVDDPTTIPPTTTTTTTTTTTTTTTTTTTTTITDSRAGEGSIKAVDHAIVG 360
DB 319 VGKASDYMLYVDDPTTIPPTTTTTTTTTTTTTTTTTTTTTITDSRAGEGSIKAVDHAIVG 378
QY 361 GVAVVVFAMLCIIILIGRYFARHKGTYFTHKAGADDAADDAADTAIINAEAGGONNSEKK 420
DB 379 GVAVVVFAMLCIIILIGRYFARHKGTYFTHKAGADDAADDAADTAIINAEAGGONNSEKK 438
QY 421 EYF 423
DB 439 EYF 441

RESULT 4

US-09-866-028-61
Sequence 61, Application US/09866028
Patent No. 6642360
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Fliszaroff, Ellen
APPLICANT: Gerdtisen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kljavin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/866,028
CURRENT FILING DATE: 2001-05-25
Prior application data removed - consult PAM or file wrapper
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LENGTH: 440
TYPE: PRI
ORGANISM: Homo Sapien
US-09-866-028-61

Query Match 97.8%; Score 2149; DB 4; Length 440;
Best Local Similarity 98.3%; Pred. No. 7.2e-183;
Matches 416; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

1 AAPGRLRLILLLLSAALLIPTGDSQNLFTKDVIVIEGEVATISGVNKSDDSVIQLN 60
19 AAPPG--LRLLILLSAALLIPTGDSQNLFTKDVIVIEGEVATISGVNKSDDSVIQLN 76
61 PRRQTIYFDFRPLKDSRFQNLNFSSELSKSLTNVSIISDEGRYFCQLYTDPQESYTTI 120
77 PRRQTIYFDFRPLKDSRFQNLNFSSELSKSLTNVSIISDEGRYFCQLYTDPQESYTTI 136
121 TTVPRRNIMIDIOKTAVEGEIEVNCATMAASKPATITRMFGKNTLKGKSEVEMSDM 180
137 TVVPRRNIMIDIOKTAVEGEIEVNCATMAASKPATITRMFGKNTLKGKSEVEMSDM 196
181 YVTSQMLKVNKEDDGVPIYCOVEHPAVTGNLQTORYLEVOYKPCVHIQMTYPLQGLTR 240
197 YVTSQMLKVNKEDDGVPIYCOVEHPAVTGNLQTORYLEVOYKPCVHIQMTYPLQGLTR 256
241 EGAPFELTCALGKPOVMTWTRVVDENPOHNVLSGNPLFINLNKNTNGYRCASNI 300
257 EGAPFELTCALGKPOVMTWTRVVDENPOHNVLSGNPLFINLNKNTNGYRCASNI 316
301 VGSASDVMYVYDPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 360
317 VGSASDVMYVYDPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 376
361 GVAVAVVAVFAMCLIIIGRYFAHKGTYFTHAKGADDAADTAIINAGGONNSEEEK 420
377 GVAVAVVAVFAMCLIIIGRYFAHKGTYFTHAKGADDAADTAIINAGGONNSEEEK 436
421 EYF 423
437 EYF 439

RESULT 5
US-08-659-984A-5
Sequence 5, Application US/08659984A
Patent No. 5942400
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Sinha, Sukanto
APPLICANT: Jacobson-Croak, Kirsten L.
TITLE OF INVENTION: Assays for Detecting Beta-Secretase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,984A
FILING DATE: 07-JUN-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002810US
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-659-984A-5

Query Match 41.1%; Score 904; DB 2; Length 444;
Best Local Similarity 44.7%; Pred. No. 4.2e-72;
Matches 194; Conservative 74; Mismatches 136; Indels 30; Gaps 7;

13 LLLAAA---LIPGDSQNLFTKDVIVIEGEVATISGVNKSDDSVIQLNPNQTIYFR 69
17 LLLQAAAKNVKKSQGGPFLQNVIVIEGEVATISGVNKSDDSVIQLNPNQTIYFR 76
70 DFRPLKDSRFQNLNFSSELSKSLTNVSIISDEGRYFCQLYTDPQESYTTITVLPPEL 129
77 DKALRDRIRIELVNASWHELSISVDVSLSDGQYCSLFMPVKTSKAYLTVLGVPEKP 136
130 MIDIOKTAVEGEIEVNCATMAASKPATITRMFGKNTLKGKSEVEMSDM---DVTYTSQ 186
137 QISGSPVPMGDMQLCTCKTSGSKPADIIRFNDKEIKVKYKLEBDANKRTFTVYST 196
187 LMLKVNKEDDGVPIYCOVEHPAVTGNLQ--TORYLEVOYKPCVHIQMTYPLQGLTR 245
197 LDFRVDSDDEVAVICRDHESLNATPQVAMQVEIHHTPSVKL---IPSPFQEGQPL 253
246 ELTCALGKPOVMTWTRVVDEN--POHNVLSGNPLFINLNKNTNGYRCASNIYVK 303
254 ILTCSKSKPLPEPVLTKDGELEPDRMVVSGRELNLPLNKTNGYRCASNIYVK 313
304 AHSQVYVYDPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 349
314 SAEVYLVHVDVPTLPTTIIIPSLITATVTTVAITTSPTTSATSSIRDPNMLAGNG 373
350 TIGAVDVAIVGVAVVAVFAMCLIIIGRYFAHKGTYFTHAKGADDAADTAIINA 409
374 P---DHALIGIVAVVAVFAMCLIIIGRYFAHKGTYFTHAKGADDAADTAIINA 429
410 EGGONNSEEEKYF 423
430 EGGONNSEEEKYF 443

RESULT 6
US-08-660-531-5
Sequence 5, Application US/08660531
Patent No. 6221645
GENERAL INFORMATION:
APPLICANT: Chrysler, Susanna M.S.
APPLICANT: Sinha, Sukanto
APPLICANT: Keim, Pamela S.
APPLICANT: Anderson, John P.
TITLE OF INVENTION: Beta-Secretase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,531
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,498
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002210US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-660-531-5

Query Match 41.1%; Score 904; DB 3; Length 444;
Best Local Similarity 44.7%; Pred. No. 4,2e-72;
Matches 194; Conservative 74; Mismatches 136; Indels 30; Gaps 7;
QY 13 LILSAANA--LITPTGQGLVFTKDVTVIGEVATISQVKNKSDSDVILNPNRQTIYFR 69
DB 17 LILQAAASKNVKGSGGQFPPLONTVYEGGTAIILTCRVQDNDNTSLQWSPAQOTLIYFD 76
QY 70 DRRPLKDSRFPOLLNFSSELKVSILTNVSIISDEGRYFCQLYDPPQESYTTITVLPENL 129
DB 77 DKALARDNRIELVRSWHELSISVSDVSLSDGQYTCSLFTVPVTKSAVILTVGVPEKP 136
QY 130 MIDIQDVAEESSEVNCTAMASKPATIRFKNKELKGSVEEMS--DWTYVTSQ 186
DB 137 QISGESSVMEGDLQILTKTISGSKPADIRFKNDKEIKDYKYLKEEDANKRTFTVST 196
QY 187 LMLKVKHEDGVPIVCOVEHPAVTGNLQ--TORYLEVOYKPOVNIOMTYPLQGLTREGDAF 245
DB 197 LDFRVDRSDGVAVICRVVHESLNATPOVAMQVLEIHTPSVKI--IPSTPPQEGGPL 253
QY 246 ELTCEALIGKPOVMTWVRVDEM--POHAYLSGNLFINNLTNDGTYRCEASNIYVK 303
DB 254 ILTCKSGKPLPEPLMTKDGELDPDRMVVSGELNLLPLNKTDNGTYRCEATNTIGQ 313
QY 304 AHSQVNLVYDPPPTIIPPTITTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 349
DB 314 SAAEVLIVHDVYVNTLLPTTIIIPSLTAVTTVAITTSPTTSATTSIRDPNLAQNG 373
QY 350 TIGAVDHAIVGVAVVYVPAULCLIIIGRFARHKGYTFTHAKGADADAADATAIINA 409
DB 374 P---DHALIGGIIVAVVVFVTLCSIFLLGRYLARKKGYLTINTEAKGADADADATAIINA 429
QY 410 EGGQNNSEKKEKF 423
DB 430 EGSQVNAEKEKF 443

RESULT 7
US-08-659-984A-1
; Sequence 1, Application US/0865984A

Patent No. 5942400
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Sima, Sukanto
APPLICANT: Jacobson-Croak, Kirsten L.
TITLE OF INVENTION: Assays for Detecting Beta-Secretase
TITLE OF INVENTION: Inhibition
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,984A
FILING DATE: 07-JUN-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002210US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-659-984A-1

Query Match 40.7%; Score 893.5; DB 2; Length 421;
Best Local Similarity 45.0%; Pred. No. 3.3e-71;
Matches 188; Conservative 73; Mismatches 130; Indels 27; Gaps 6;
QY 26 GQNLFTKDVTVIGEVATISQVKNKSDSDVILNPNRQTIYFRDPRPLKDSRFPOLLNFS 85
DB 10 GQFPLTQNTVYEGGTAIILTCRVQDNDNTSLQWSPAQOTLIYFDXKALRDRRIELVRS 69
QY 86 SSELKVSILTNVSIISDEGRYFCQLYDPPQESYTTITVLPENLMIDIOKDAVGEEL 145
DB 70 WHELSISVSDVSLSDGQYTCSLFTVPVTKSAVILTVGVPEKPOISGESSVMEGDLMO 129
QY 146 VNCTAMASKPATIRFKNKELKGSVEEMS--DWTYVTSQMLKVKHEDDGVPIVC 202
DB 130 LTKCKSGKPADIRFKNDKEIKDYKYLKEEDANKRTFTVSTLDFRVDRDDGVAVIC 189
QY 203 QVEHPAVTGNLQ--TORYLEVOYKPOVNIOMTYPLQGLTREGDAFELTCEALIGKPOVMT 261
DB 190 RVHESLNATPOVAMQVLEIHTPSVKI--IPSTPPQEGGPLILTKCKSGKPLPEPLV 246
QY 262 WVRVDEM--POHAYLSGNLFINNLTNDGTYRCEASNIYKSAHSDYVNLVYDPPPTI 319
DB 247 WTKDGELDPDRMVVSGELNLLPLNKTDNGTYRCEATNTIGOSSAAEVLIVHDVYVNTL 306
QY 320 PPTTT 365
DB 307 LPTTIIIPSLTAVTTVAITTSPTTSATTSIRDPNLAQNGP---DHALIGGIIVAV 362
QY 366 VVPAULCLIIIGRFARHKGYTFTHAKGADADAADATAIINAGQNNSEKKEKF 423

Db 363 VVFVLLCSIFLLGRYLARKKGYLTNEAKGADPADADTAIINAGSQVNAEKEKEYF 420

RESULT 8

US-08-660-531-1
 ; Sequence 1, Application US/08660531
 ; Patent No. 6221645
 ; GENERAL INFORMATION:
 ; APPLICANT: Chrysler, Susanna M.S.
 ; APPLICANT: Sinha, Sukanto
 ; APPLICANT: Keim, Pamela S.
 ; APPLICANT: Anderson, John P.
 ; TITLE OF INVENTION: Beta-Secretase
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Ctr., 8th Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/660,531
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/480,498
 ; FILING DATE: 07-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Heeslin, James M.
 ; REGISTRATION NUMBER: 29,541
 ; REFERENCE/DOCKET NUMBER: 15270-002210US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-326-2400
 ; TELEFAX: 415-326-2422
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 421 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-660-531-1

Query Match 40.7%; Score 893.5; DB 3; Length 421;
 Best Local Similarity 45.0%; Pred. No. 3.3e-71;
 Matches 188; Conservative 73; Mismatches 130; Indels 27; Gaps 6;

QY 26 GQNLFTKDVTVIEGEVATISCOVNSDDSVIQLNPNRQTIYFRDPRPKDSRFPOLLNFS 85
 DB 10 GGPPLQNTVVEGGVAILTCRDQNDNTSLQMSNPACQTLFYDDKKALRDRIRIELVPAAS 69
 QY 86 SSELKATLTVNSISDEGRYFCOLYTPPOESYTTIVLVRPNMLMDIOKDAVEGEIE 145
 DB 70 WHELSISVSDVLSDEGQYTCSTFTMPVKTSKAYLTVLGVPEKPOLSGSSSVWGGDLMO 129
 QY 146 VNCTAMASKPATTTIRFKGNKEIKGKSEVEEWS--DNYTTSQMLKVNKEDDGVPIYC 202
 DB 130 LTKCKTSGSKPADIRFVKDKDKIKDKVYLKEDANRKYTFVASTLDPRVRSDDGVAVIYC 189
 QY 203 QVNHPAVTNLQ--TQVYLEVQYKQVNIQMTYRPLQGLTREGEAFELTCALIGKQRPVWT 261
 DB 190 RVDHESLMTPOVAMOVLEIHTPSVKI--IPSTPPEGGPLITLTCSSKSKPLRBPVL 246
 QY 262 WRAVDDDM--PQHAVLSGNLFINLNKNTDNGTYRCEASNIIVGKASHDYMLVYDPPPTI 319
 DB 247 WTKDGGELDPDRMVVSGRELNLTLFNKTDNGTYRCEANTITIGSSASAEVLLVHDVPNTL 306

QY 320 PPTTTTTTTTTTTTTTTTTT-----DSRAGEEGTIGAVDHAVIGVAV 365
 DB 307 LPTTIISLTATVTTTVAITTSPTTSATTSIRDPNALAGQNP-----DHALIGLIVAV 362
 QY 366 VFPAMLCILITIGYFPAHKGTFTTHAKGADDAADTAIINAGSQVNAEKEKEYF 423
 DB 363 VVFVLLCSIFLLGRYLARKKGYLTNEAKGADPADADTAIINAGSQVNAEKEKEYF 420

RESULT 9

US-09-778-510-4
 ; Sequence 4, Application US/09778510
 ; Patent No. 6512095
 ; GENERAL INFORMATION:
 ; APPLICANT: Baum, Peter
 ; TITLE OF INVENTION: Molecules Designated B7L1
 ; FILE REFERENCE: 2844-US
 ; CURRENT APPLICATION NUMBER: US/09/778,510
 ; PRIOR FILING DATE: 2001-02-07
 ; PRIOR APPLICATION NUMBER: PCT/US99/17906
 ; PRIOR FILING DATE: 1999-08-05
 ; PRIOR APPLICATION NUMBER: 60/095,663
 ; PRIOR FILING DATE: 1998-08-07
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO: 4
 ; LENGTH: 398
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; US-09-778-510-4

Query Match 33.6%; Score 738.5; DB 4; Length 398;
 Best Local Similarity 38.8%; Pred. No. 1.9e-57;
 Matches 165; Conservative 73; Mismatches 136; Indels 51; Gaps 9;

QY 12 LLLSAAALPTG-----DQNLFTKDVTVIEGEVATISCOVNSDDSVIQLNPNRQTI 66
 DB 11 LLLLLASNAAGANLQDSDSQPWTSDETVAGGVTLKQVNDHESSIQMSNPACQTL 70
 QY 67 YFRDPRPKDSRFPOLLNFSSELKVSITNVISDEGRYFCOLYTPPOESYTTIVLVRP 126
 DB 71 YFGKRALRDRIRIELVSTHSLISISNVALADEGEYTCSTFTMPVKTAKSLVTVLGIP 130
 QY 127 RNLMIDIOKDAVEGEIEVNCTAMASKPATTTIRFVKGNKEIKG--KSEVEEWS--NYTV 183
 DB 131 QPILITGKSLRKEKETATLNCSSGSKPAAQLTRKGDDELHGDRTRIODEDPYKTFIV 190
 QY 184 TSQMLKVNKEDDGVPIYCOVNHPAVTG--NLQTORYLEVQYKQVNIQMTYRPLQGLTR 242
 DB 191 SSVSFGVTRRDDGAINVCSVNHSLKGAADRSTQRIEVLVYTPAMLR---PEPAHREG 247
 QY 243 DAFELTCEALGKPPVAVTVRVDDEMP---QHAVLSGNLFINLNKNTDNGTYRCEAS 298
 DB 248 QKLLHCEGSGNPVQGYVWVWKGSEPPLMQTESALIFP-----FLNKSDSGYGCAT 302
 QY 299 NIVGKASHDYMLVYDPPPTIIPPTTTTTTTTTTTTTTTTTTINDSRAGEEGTIGAVNHAV 358
 DB 303 SNMGSYATVFLANNDS---PVSSSSSTV-----HAI 332
 QY 359 IGVVAVVVPAMLCILITIGYFPAHKGTFTTHAKGADDAADTAIINAGSQVNAEKE 418
 DB 333 IGGIVAFIVPALLILIFLGHYLRHKGYLTTHAKGSDPADADTAIINAGSQVNSGDD 392
 QY 419 KKEYF 423
 DB 393 KKEYF 397

RESULT 10
 US-09-778-510-6
 ; Sequence 6, Application US/09778510
 ; Patent No. 6512095
 ; GENERAL INFORMATION:

APPLICANT: Baum, Peter
TITLE OF INVENTION: Molecules Designated B7L1
FILE REFERENCE: 2844-US
CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: PCT/US99/17906
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: 1999-60/095,663
PRIOR FILING DATE: 1999-08-07
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO: 6
LENGTH: 398
TYPE: PRT
ORGANISM: Homo sapien
US-09-778-510-6

Query Match 33.3%; Score 732.5; DB 4; Length 398;
Best Local Similarity 38.3%; Pred. No. 6,5e-57;
Matches 162; Conservative 74; Mismatches 144; Indels 43; Gaps 8;

QY 10 LLLLLLSAALIPFG-----DQNLFTKDVYIEGEVATISGVNKKSDSVIQLNPRQ 64
DB 9 LLLLLLFAACWAPGAGNLSQDSDQPTSDETVVAAGTVLKCQVNDHEDSSLOWSNPAQ 68
QY 65 TIYFRDPRFKDSRFOLNFSSELKVSILTNVSISSDEGRYFCOLYTDPPQESYTTITLV 124
DB 69 TIYFGKRALRDRNRQIVTSTPHELSISNVALADEGEYTCISFTMPVTRAKSLVTVLG 128
QY 125 PPRNIMIDIQKDAVEGEIEVNCCTAMASKPATTTIRWKNELKKGK-SEVEWSD--MY 181
DB 129 IPQKPIITGKSSLRKQDTATLNCSSGSKPAPARLTWRKGDDEHGEPTRIQEDPNKTF 188
QY 182 TVTSOLMKVHKEDGVPIQVEHPAVTG-NLQTRKLEYQKQVHIQWTPVPLQGLTR 240
DB 189 TVSSSVTTQVTRVEDGASIVCSVNHESLKGADRSISQILEVLYPTAMIRDDP---HPR 245
QY 241 ESDAEELTCEALGKEQPVWTVVRVDEMPOHVAVLGNNLFINNKTKDNGTYCEASNT 300
DB 246 EGQKLLHCEGRGNPVCQYWEK-EGSVPLKMQESALIFPPLNKSDSGTYCTATSN 304
QY 301 VKKASDVMVLYYDDPTTTPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 360
DB 305 MCSYKAYVYTLVNDPS---PVSSSSSTY-----HAILG 334
QY 361 GVAVAVVPMCLLILGRYFARHKGTYFTHEKAGDADAADATAIINAEGGONNSEBK 420
DB 335 GIVAFIVFLILMLIFLGHYILRHKGTYLTHAKGSDAPADPATIINAEGGQSGDDKX 394
QY 421 EYF 423
DB 395 EYF 397

RESULT 11
US-09-907-794A-84
Sequence 84, Application US/09907794A
Patent No. 6635468
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.
APPLICANT: Hillen, Kenneth, J.
APPLICANT: Kijavlin, Ivar U.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tomas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,794A
PRIOR FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO: 84
LENGTH: 398
TYPE: PRT
ORGANISM: Homo sapiens
US-09-907-794A-84

Query Match 33.3%; Score 732.5; DB 4; Length 398;
Best Local Similarity 38.3%; Pred. No. 6,5e-57;
Matches 162; Conservative 74; Mismatches 144; Indels 43; Gaps 8;

QY 10 LLLLLLSAALIPFG-----DQNLFTKDVYIEGEVATISGVNKKSDSVIQLNPRQ 64
DB 9 LLLLLLFAACWAPGAGNLSQDSDQPTSDETVVAAGTVLKCQVNDHEDSSLOWSNPAQ 68
QY 65 TIYFRDPRFKDSRFOLNFSSELKVSILTNVSISSDEGRYFCOLYTDPPQESYTTITLV 124
DB 69 TIYFGKRALRDRNRQIVTSTPHELSISNVALADEGEYTCISFTMPVTRAKSLVTVLG 128
QY 125 PPRNIMIDIQKDAVEGEIEVNCCTAMASKPATTTIRWKNELKKGK-SEVEWSD--MY 181
DB 129 IPQKPIITGKSSLRKQDTATLNCSSGSKPAPARLTWRKGDDEHGEPTRIQEDPNKTF 188


```

APPLICANT: Ford, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902, 775A
CURRENT FILING DATE: 2001-07-10
PRIORITY APPLICATION NUMBER: PCT/US00/04414
PRIORITY FILING DATE: 2000-02-22
PRIORITY APPLICATION NUMBER: US 60/143, 048
PRIORITY FILING DATE: 1999-07-07
PRIORITY APPLICATION NUMBER: US 60/145, 698
PRIORITY FILING DATE: 1999-07-26
PRIORITY APPLICATION NUMBER: US 60/146, 222
PRIORITY FILING DATE: 1999-07-28
PRIORITY APPLICATION NUMBER: PCT/US99/20554
PRIORITY FILING DATE: 1999-09-08
PRIORITY APPLICATION NUMBER: PCT/US99/20944
PRIORITY FILING DATE: 1999-09-13
PRIORITY APPLICATION NUMBER: PCT/US99/21090
PRIORITY FILING DATE: 1999-09-15
PRIORITY APPLICATION NUMBER: PCT/US99/21547
PRIORITY FILING DATE: 1999-09-15
PRIORITY APPLICATION NUMBER: PCT/US99/23089
PRIORITY FILING DATE: 1999-10-05
PRIORITY APPLICATION NUMBER: PCT/US99/28214
PRIORITY FILING DATE: 1999-11-29
PRIORITY APPLICATION NUMBER: PCT/US99/28313
PRIORITY FILING DATE: 1999-11-30
PRIORITY APPLICATION NUMBER: PCT/US99/28564
PRIORITY FILING DATE: 1999-12-02
PRIORITY APPLICATION NUMBER: PCT/US99/28565
PRIORITY FILING DATE: 1999-12-02
PRIORITY APPLICATION NUMBER: PCT/US99/30095
PRIORITY FILING DATE: 1999-12-16
PRIORITY APPLICATION NUMBER: PCT/US99/30911
PRIORITY FILING DATE: 1999-12-20
PRIORITY APPLICATION NUMBER: PCT/US99/30999
PRIORITY FILING DATE: 1999-12-20
PRIORITY APPLICATION NUMBER: PCT/US00/00219
PRIORITY FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 84
LENGTH: 398
TYPE: PRT
ORGANISM: Homo sapiens
US-09-902-775A-84
Query Match 33.3%; Score 732.5; DB 4; Length 398;
Best Local Similarity 38.3%; Pred. No. 6.5e-57;
Matches 162; Conservative 74; Mismatches 144; Indels 43; Gaps 8
10 LLLLLLSAALPTG-----DQNFPTDVTVIGEVATISCCVKNKSDSEVILNPNQ 64
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 9 LLLLLLFAACMAFGCANLSQDDSGQWTSDETVVAGCTVYAKCYKHEDSDLSGMSVPAQ 68
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
65 TIVFRDFRLKSRFQLNFFSSSEIKVSLVNVSISSDEGRFTQCLYTDPPQESTTTTIVLV 124

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Db	69	TLVEGRKALRDNRIQLVTSIPHELSSISINVALADGEGYCSIFTMFVRFAKSLVTVLG	128
Qy	125	PRRLMIDIOKDTAVEGEIEVNTCTAAMASKPATIRPFKGNKEIKGK--SEVEWSD--MY	181
Db	129	IPQRPITTGKSSIREKDTATLNCQSSGSKPAALTYRKQDELHGEPTRIQEDPNGT	188
Qy	182	TVTSQMLKVKHKEDDGVVVICQVEHPAVTG--NIOTORYLEVQYPOVHIQMTYPLQGLTR	240
Db	189	TVSSSVTFQVYREDDGASIVCSVNHESLKGADRTSORIEVLYPTPMIRDPF---HPR	245
Qy	241	EGDAFELTCEALIGPOQVMTYTWAVDDEMPHVALSGPNFINNLNTIDNGTYCEASNI	300
Db	246	EGQILLHCEGRGPNVPOQYIMEK--EGSVPLKMTQSALIFPPLNKSDSGTYGCTATSN	304
Qy	301	VGKASHDYMLYVXPPTTIPETITTTTTTTTTTTTTTTTTLITDSRAGEGTTGAVDHA	360
Db	305	MGSKAYVYTLNVNDPS---PVPSSSTY-----HALIG	334
Qy	361	GVAVVVPFANLCLIIIGRFPAARKGTITYTEAKGADDAADPATIINAEGGNNSEBK	420
Db	335	GIVAFIVFELLIMLIFLGHYLRKRGTYLTHEAKGSDPADPATIINABEGSGGDDXK	394
Qy	421	EFYF	423
Db	395	EFYF	397

RESULT 14
 US-09-778-510-2
 ; Sequence 2, Application US/09778510
 ; Patent No. 6512095
 ; GENERAL INFORMATION:
 ; APPLICANT: Baum, Peter
 ; TITLE OF INVENTION: Molecules Designated B7L1
 ; FILE REFERENCE: 2844-US
 ; CURRENT APPLICATION NUMBER: US/09/778, 510
 ; CURRENT FILING DATE: 2001-02-07
 ; PRIOR APPLICATION NUMBER: PCT/US99/117906
 ; PRIOR FILING DATE: 1999-08-05
 ; PRIOR APPLICATION NUMBER: 66/095, 663
 ; PRIOR FILING DATE: 1998-08-07
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 432
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-09-778-510-2

Query Match	32.6%;	Score 715.5;	DB 4;	Length 432;
Best Local Similarity	36.1%;	Pred. No. 2.4e-55;		
Matches 165;	Conservative 75;	Mismatches 140;	Indels 77;	Gaps 10;

Qy	10	LLLLLSAALLIFG---DG---QNL-----F	30
Db	9	LLLLLIFACWAPGAGANLSCDGYWQEODLIELGTIAPLDEAISSTWSSPDMLASQSQPW	68
Qy	31	TKDVTYVEGEVATISCCVANKSDSDSVIOLINPNROTIYRDRPRPKDSRFOLNFFSSSLX	90
Db	69	TSDETVVAGGTIVLKCQYKHEDSSLSQNSPFAQDTIYGEGRALRDNRIQLVTSIPHEL	128
Qy	91	VSLTNVSIISDEGRYFCQLYTDPPQSSYTTITVIVPPRNLMIDIOKDTAVEGEIEVNTCTA	150
Db	129	ISISVNLADGEGYCSIFTMFVRFAKSLVTVLGIPQRPITTGKSSIREKDTATLNCQ	188
Qy	151	MASKPATIRPFKGNKEIKGK--SEVEWSD--MYTVNSQMLKVKHKEDDGVVVICQVEHP	207
Db	189	SGSKPAALTYRKQDELHGEPTRIQEDPNKCTFVSSSVTFQVYREDDGASIVCSVNH	248
Qy	208	AVTG--NIOTORYLEVQYPOVHIQMTYPLQGLTREGDAFELTCEALIGKPOQVMTYTWAVD	266
Db	249	SLKGDARETSQRIVLYPTPMIRDPF---HPRGQILLHCEGRGPNVPOQYIMEK--E	304

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QY 267 DEPCGAVLSGPNLFNNLNKNDNGTYRCEASNIYKASHDMLVYDPEPTTTPPTTT 326
DB 305 GSVPLKMTQESALIFPFLNKSDSGTYCTATSNMGSYKAYTLNVNDPS--PVPSSSS 361
QY 327 TTTTTLTTLITDSRAGEGTGAVDHAIVGVAVVAVPAMCLITIGRYFARKHG 386
DB 362 TV-----HAIIGGVAIVLVLLIMLITFLGHYLRHKG 394
QY 387 TYTFHEAKADDAADDAIINAEGGONNSEKKEYF 423
DB 395 TYLTHEAKGSDPADADTAIINAEGGSGDDKKEYF 431

RESULT 15
US-09-205-258-947
; Sequence 947, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,992
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,883
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,897
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,898
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 947
LENGTH: 227
TYPE: PRT
ORGANISM: Homo sapiens
US-09-205-258-947

Query Match 15.2%; Score 333; DB 4; Length 227;
Best Local Similarity 33.3%; Pred. No. 9.8e-22;
Matches 77; Conservative 49; Mismatches 97; Indels 8; Gaps 5;

QY 88 ELKSLTNVSIISDEGRYFCQLYTDPPQESYTTITVLPNNLMIDIOKTAIVEGELEVN 147
DB 1 ELSISINVALADGEYTCISIFTPVATKSLVTLGIPKPIITGVKSLRDXDTATLN 60
QY 148 CTMAASKPATTIIPFKNKELKQK-SVEEWSMD--WYVTSQMLKYNKREDDGVPIYCOV 204
DB 61 QSSGSKPAPRLTWKQDQELHGFRTIQDPYKTFVSSVTFQVTRDDGASIVCSV 120
QY 205 EHPAVTG-NIQGTQRYLEVCYKPCVNIQMTYPLQGLTFREGDAFELTCAIGKPOPVWTVW 263
DB 121 NHESLKADASTISGRIVLVTPATMIRPDP--HPRGCKLLHCGRGNPVPQQLWE 177
QY 264 RVDDEMPQHAVLSGPNLFNNLNKNDNGTYRCEASNIYKASHDMLVYDPEPTTTPPTTT 326
DB 178 K-EGSVPLKMTQESALIFPFLNKSDSGTYCTATSNMGSYKAYTLNVND 227
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Search completed: July 7, 2004, 06:05:19
Job time : 35.2312 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 7, 2004, 05:56:13 ; Search time 33.7249 Seconds

(without alignments)
1260.692 Million cell updates/sec

Title: US-10-622-237-2

Perfect score: 2283
Sequence: 1 MASVLPFGSGCCAAAAA.....AIIINAGGQNNSEKKEYFI 442

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR 78:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	268	11.7	407	2 T08732	hypothetical prote
2	263.5	11.5	5175	2 T20992	hypothetical prote
3	263.5	11.5	5198	2 T43290	hemichitin precurs
4	248	10.9	518	2 UC4024	poliovirus recepto
5	247.5	10.8	530	2 A53437	poliovirus recepto
6	244	10.7	417	2 A44194	poliovirus recepto
7	244	10.7	467	1 HIMS3	poliovirus recepto
8	243	10.6	725	2 JEO099	neural cell adhesi
9	242.5	10.6	538	2 T68093	PRR2 delta - human
10	241.5	10.5	392	2 B44194	poliovirus recepto
11	240	10.5	392	1 RMHUPD	poliovirus recepto
12	240	10.5	417	1 RMHUPA	poliovirus recepto
13	239	10.5	1088	1 IJXLNL	neural cell adhesi
14	230.5	10.1	4162	2 T42633	connectin/citin -
15	230	10.1	344	2 I56551	neurotrophin - rat
16	226	9.9	812	2 B42632	cell adhesion mole
17	226	9.9	932	2 A42632	cell adhesion mole
18	225	9.9	7962	2 I38346	elastic titin - hu
19	223.5	9.8	1011	2 T13669	neuromusculin - fr
20	223	9.8	725	2 JEO100	neural cell adhesi
21	223	9.8	1092	1 JN0635	neural cell adhesi
22	222	9.7	478	2 I53960	PRR2 alpha - human
23	218.5	9.6	345	2 S03199	opioid-binding pro
24	218.5	9.6	588	2 A45254	surface glycoprote
25	217	9.5	588	2 JH0506	adhesion molecule
26	216.5	9.5	345	2 UC4025	opioid-binding cel
27	216	9.5	765	2 C42632	cell adhesion mole
28	214	9.4	4391	2 A38096	perlecan precursor
29	210.5	9.2	345	2 UC1239	opioid-binding pro

30	209.5	9.2	584	2 I50419	s-glycerin precursor
31	209	9.2	336	2 JCS519	50K glycoprotein p
32	206	9.0	702	2 A56319	carcinoembryonic a
33	205.5	9.0	338	2 UC4776	limbic-system-asso
34	205.5	9.0	646	2 I38049	cell surface glyco
35	204.5	9.0	338	2 JCI238	opioid-binding pro
36	204	8.9	3707	2 I58252	heparan sulfate pr
37	203	8.9	1323	2 P05568	connectin 3B - chi
38	202.5	8.9	862	2 I49583	differentiation an
39	202.5	8.9	868	2 A46312	CD22 homolog/B 1ym
40	202	8.8	847	2 JH0371	B-cell adhesion pr
41	202	8.8	1443	2 I50600	neogenin - chicken
42	199.5	8.7	1241	2 T37190	nephrin - human
43	197	8.6	583	2 I39428	alcam - human
44	196	8.6	1091	1 IJCXNL	neural cell adhesi
45	195.5	8.6	1612	2 T30805	ductal protein - mo

ALIGNMENTS

RESULT 1
T08732
Hypothetical protein DKFZps66B0846.1 - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
C/Accession: T08732
R/Ottensmeyer, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A/Reference number: Z16474
A/Accession: T08732
A/Molecule type: mRNA
A/Residues: 1-407 <OT>
A/Cross-references: EMBL:AL050071
A/Experimental source: fetal kidney; clone DKFZps66B0846
A/Note: DKFZps66B0846.1

Query Match 11.7%; Score 268; DB 2; Length 407;
Best Local Similarity 26.7%; Pred. No. 1.4e-11;
Matches 84; Conservative 60; Mismatches 123; Indels 48; Gaps 13;

QY	120	GRYFCQLYDP--PQESYTTITVLPVPRNLMIDQKQTVABG--EELEVNTAMASRPAT 175
DB	2	GKTYCKAVTFPLGNAQSSITVTVLVEPTVSLIK-GPDSLIDGNETVAACIATGKPPVA 60
QY	176	TIRPFKNTTELKGSSEVEWSDMY-----TTSQMLKHKEDDGVVICQVEHPAVTGN 230
DB	61	HIDW-EGDL-----GWESESTTSFPNEMATIIISQYKLPTRFRAGRRIITCVKHPALEKD 114
QY	231	LQTORYLEVOYKPPQVYHQMTPYLOGLTRGDALFLTEAIGKPPQPVATVWRVDENPQH 290
DB	115	IRYFIDIDIQAPPEVSVTGDMFWGVRKG--VNLKCNAPANDPFFKSVSRDLGQWPDG 172
QY	291	AVLGGPML-FNNNNKTDNGTYRCEASNIIVGAKSDVWLIVYDPP--TTIP-----PTT 342
DB	173	LLAADNTHFVHPTFTWVSQYICKVNSLQGRSDQVYIISDPPTTTTIOPTIQMPST 232
QY	343	TTTTTTTT-----TTTITITTSRAGEBGSIRAVDAVIGVAVVVFAMLCILI- 393
DB	233	ADIEDLATPEPKLPFPSTIATII-----KDTIATIIISVVGALFIVLVSIAIGFC 265
QY	394	-----ILGRYFAKH 402
DB	286	YRRRTTRGDYFAKH 300
RESULT 2		
T20992		
Hypothetical protein F1509.4a - Caenorhabditis elegans		
C/Species: Caenorhabditis elegans		
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000		
C/Accession: T20992; T24733		

R/Sulton, J.
submitted to the EMBL Data Library, December 1994
A/Reference number: Z19355
A/Accession: T20992
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-5175 <M1>
A/Cross-references: EMBL:Z47068, PIDN:CAA87335.1, GSPDB:GN00028, CESP:FL15G9.4a
A/Experimental source: clone F15G9
R/Kershaw, J.
submitted to the EMBL Data Library, December 1994
A/Reference number: Z19929
A/Accession: T24733
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-5175 <M1>
A/Cross-references: EMBL:Z47070, PIDN:CAA87344.1, GSPDB:GN00028, CESP:FL15G9.4a
A/Experimental source: clone T09B9
C/Genetics:
A/Map position: X
A/Intons: 85/1, 120/1, 334/3, 370/1, 477/2, 606/3, 664/1, 935/3, 977/1, 1051/3, 1184/3, 1251/2, 2593/3, 2699/3, 2759/1, 2889/3, 2913/3, 2941/1, 2967/3, 2991/3, 3033/1, 4225/1, 4361/1, 4408/1, 4456/1, 4498/1, 4647/3, 4838/1, 4879/1, 4941/1, 5011/1, 5077/1
Query Match 11.5%; Score 263.5; DB 2; Length 5175;
Best Local Similarity 24.6%; Pred. No. 7.6e-10;
Matches 87; Conservative 66; Mismatches 129; Indels 71; Gaps 15;
QY 52 VTVIEGEVATISQVKNKSDSVIQLNPNRQITYPDFRPL---KDSFPQLNBSSEL 107
DB 2200 VTAIKGALPFCPIP-D DK-----NFKQIIMLNPNOPIDLEADDAITRL---SND 2249
QY 108 KVALTVNSIDEGRYCOLYTPDPSYR-TITVLPNPNLMIDIKD-TAVEGEIEVN 165
DB 2250 RLTLNLTENDEQYSCRKNDAGENSFPKATVLPPIITIMDKDKNTAHEHSTVLS 2309
QY 166 CTAMASKPATITRMFKG-----NTELKGSVEEWSDMYTVTSQMLKVKH 211
DB 2310 CPA-TGKRPEDITMFKDGEAIIHENIADIIPNGLNG-----NQLKITRIK 2354
QY 212 EDGCVPIQCVHPATYGNLQYRYEYQKPYVH---IQMYPIQLGRLREGDALELCE 268
DB 2355 EGAGKXTCADNSA--GSVEQDVNNAVITTPKIEKDGIPSDYEQ---QNERVVISCP 2408
QY 269 AIGKPPVMTVYWRVDDENPQHAVL-----SGPNLFINNINKTNGYRCEASNIYKAS 324
DB 2409 VYARP-PAKITWIKAGKPLQSDKFKVTSANGQLYFKLRETDSKYTCIATNEAGTDKR 2467
QY 325 DYNLYVYDPTTTP-----PTTTTITTTTITTTITTTITTSRAGE 365
DB 2468 DFKVSMLVAPSPDEFNIVRITVNSGNPSTLHCAPAKGSPSTITWLDGNAL 2520

RESULT 3
T43290
hemiscentin precursor - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000
C/Accession: T43290; T20993; T24734
R/Vogel, B.E.; Hedgecock, E.M.
submitted to the EMBL Data Library, June 1998
A/Description: Hemiscentin is required for hemidesmosome mediated cell adhesion and germ-
A/Reference number: Z23596
A/Accession: T43290
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-5198 <VO>
A/Cross-references: EMBL:AF074901, PIDN:AAC26792.1
R/Sulton, J.
submitted to the EMBL Data Library, December 1994
A/Reference number: Z19355
A/Accession: T20993

A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-5198 <M1>
A/Cross-references: EMBL:Z47068, PIDN:CAA87336.1, GSPDB:GN00028, CESP:FL15G9.4b
A/Experimental source: clone F15G9
R/Kershaw, J.
submitted to the EMBL Data Library, December 1994
A/Reference number: Z19929
A/Accession: T24734
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-5198 <M1>
A/Cross-references: EMBL:Z47070, PIDN:CAA87345.1, GSPDB:GN00028, CESP:FL15G9.4b
A/Experimental source: clone T09B9
C/Genetics:
A/Map position: X
A/Intons: 85/1, 120/1, 334/3, 370/1, 477/2, 606/3, 664/1, 935/3, 977/1, 1051/3, 1184/3, 1251/2, 2593/3, 2699/3, 2759/1, 2889/3, 2913/3, 2941/1, 2967/3, 2991/3, 3033/1, 4225/1, 4361/1, 4408/1, 4456/1, 4498/1, 4647/3, 4838/1, 4902/1, 4964/1, 5034/1, 5100/1
Query Match 11.5%; Score 263.5; DB 2; Length 5198;
Best Local Similarity 24.6%; Pred. No. 7.6e-10;
Matches 87; Conservative 66; Mismatches 129; Indels 71; Gaps 15;
QY 52 VTVIEGEVATISQVKNKSDSVIQLNPNRQITYPDFRPL---KDSFPQLNBSSEL 107
DB 2200 VTAIKGALPFCPIP-D DK-----NFKQIIMLNPNOPIDLEADDAITRL---SND 2249
QY 108 KVALTVNSIDEGRYCOLYTPDPSYR-TITVLPNPNLMIDIKD-TAVEGEIEVN 165
DB 2250 RLTLNLTENDEQYSCRKNDAGENSFPKATVLPPIITIMDKDKNTAHEHSTVLS 2309
QY 166 CTAMASKPATITRMFKG-----NTELKGSVEEWSDMYTVTSQMLKVKH 211
DB 2310 CPA-TGKRPEDITMFKDGEAIIHENIADIIPNGLNG-----NQLKITRIK 2354
QY 212 EDGCVPIQCVHPATYGNLQYRYEYQKPYVH---IQMYPIQLGRLREGDALELCE 268
DB 2355 EGAGKXTCADNSA--GSVEQDVNNAVITTPKIEKDGIPSDYEQ---QNERVVISCP 2408
QY 269 AIGKPPVMTVYWRVDDENPQHAVL-----SGPNLFINNINKTNGYRCEASNIYKAS 324
DB 2409 VYARP-PAKITWIKAGKPLQSDKFKVTSANGQLYFKLRETDSKYTCIATNEAGTDKR 2467
QY 325 DYNLYVYDPTTTP-----PTTTTITTTTITTTITTTITTSRAGE 365
DB 2468 DFKVSMLVAPSPDEFNIVRITVNSGNPSTLHCAPAKGSPSTITWLDGNAL 2520

RESULT 4
JC4024
poliovirus receptor-related protein precursor - human
C/Species: Homo sapiens (man)
C/Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Nov-1999
C/Accession: JC4024
R/Lopez, M.; Eberle, F.; Matzel, M.G.; Gabert, J.; Birg, F.; Bardin, F.; Maroc, C.; Dubr
Gene 155, 261-265, 1995
A/Title: Complementary DNA characterization and chromosomal localization of a human gene
A/Reference number: JC4024, M01D:95237621, PMID:7721102
A/Accession: JC4024
A/Molecule type: mRNA
A/Residues: 1-518 <LDP>
A/Cross-references: EMBL:X76400, NID:g732795, PIDN:CAA53980.1; PID:g732795
C/Genetics:
A/Map position: X
A/Cross-references: GDB:583951
A/Map position: 11q23-11q24
C/Superfamily: poliovirus receptor; immunoglobulin homology
C/Keywords: glycoprotein; transmembrane protein
F.1-30/Domain: signal sequence #status predicted <Sig>
F.31-518/Product: poliovirus receptor-related protein #status predicted <Mat>
F.356-379/Domain: transmembrane #status predicted <TM>

F,36,72,82,139,287,308,333/Binding site: carbohydrate (Aan) (covalent) #status predicted

Query Match 10.9%; Score 246; DB 2; Length 518;

Best Local Similarity 25.4%; Pred. No. 4.9e-10;

Matches 105; Conservative 60; Mismatches 154; Indels 94; Gaps 20;

74 IQLNPRQTIYFEDFRLPKDSRFOLNFSSEELKVLTVNSISDEGRYFCQLYTDP--131

78 VAINPMGVSVALAPR-----ERVEFLRPFPTDGTILSLLEDEGVYICERATPTGQ 133

132 QESTTITVLVPPRNLMIDIQD-TAVEGEIEV--NCTAMASKPATITRMKNGTEIK 187

134 RESQNLTVAKAPTNMTEGQAVLRKKQDDKVLVATCTSANGKPSVSW--ETRLK 190

188 GKSEV--EEMSDM--YVTSQMLMKVKEDDGVPLIQVHPAVTGNLQTRY-----LE 238

191 GEAAVPGDSGTMAPVTVISRYLVPSREAHQSLACTV-----YHMKRRESULTIN 243

239 VOYKPOVHIQ--MTYPLQGLTREGDALETCENIGKPOVMTVWAVDEMPQHAVLSG 295

244 VOYEVEVTLIGFGDNWYLQEMD-----VKLTCKADANPATEYHMTTLNGLSKVGAQ 298

296 PNLFINN-LNKDTNGTCRCASNIIVGKAHSDYMLVYDPTTTPPTTTTTTTTTTTT 354

299 RILPFKGPINYSLAGYICENATPIGRSGQVEVNTIEFPYTSPE-----345

355 LITITDSRAGEEGSIRAVDAVIGVAVVAFMLCLITLIGRYFA----RH--KGYFT 408

346 ----HGRRAG-----PVTALIGVAGSI---LVLIVIGVGLVALRRRHFKDYSI 392

409 -----HEAKGA-----DPAADDTIINABGQNNSEKKE 439

393 KHAVYNGYKAGIPQHHPMAQNLQYDSDDEKKA--GPLGSSSYEEEEE 443

RESULT 5

A53437

poliovirus receptor mPVR - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000

C/Accession: A53437

R/Aoki, J.; Koike, S.; Ise, I.; Sato-Yoshida, Y.; Nomoto, A.

J. Biol. Chem. 269, 8431-8438, 1994

A/Title: Amino acid residues on human poliovirus receptor involved in interaction with F

A/Reference number: A53437; PMID:94179228; PMID:8132569

A/Accession: A53437

A/Status: preliminary

A/Molecule type: mRNA

A/Cross-references: GB:D26107; NID:9475017; PIDN:BA05103.1; PID:9825507

A/Experimental source: C57/BL6, brain

A/Note: Sequence extracted from NCBI backbone (NCBI:146664, NCBI:146677)

C/Superfamily: poliovirus receptor; immunoglobulin homology

F/4-133/Domain: immunoglobulin homology <IMM>

Query Match 10.8%; Score 247.5; DB 2; Length 530;

Best Local Similarity 22.1%; Pred. No. 5.5e-10;

Matches 91; Conservative 63; Mismatches 166; Indels 91; Gaps 14;

Db 164 IOPQSVAVARCSTGGRPARITWISSLGEAKTOQEBOIGQAGVTIISRYLVPVRAD 223

Qy 215 GYFVIGQVHEPVAATGNLQRYLEVQYKPOVHIQMTYPLQGLTREGDALETCENIGKPO 274

Db 224 GYKVCORVHESESFEPIILLPVTLSVRYPEVVIS-GYDNNWYLGRSEAI-LTCDVRSNPE 281

Qy 275 PVMVTVWVRVDEMPQHAVLISGPNLFINNLNTDNGTCRCASNIIVGKAHSDYMLVYDPT 334

Db 282 PFDYMTSTTSGVFPASAAQSGQLVHSDVKRYATTTCTTNNAVGTGACQVITVRES 341

Qy 335 TTIPPTTTTTTTTTTTTTTTTTTTTTTSDRAGEGSIKAVDAVIGGVAVV 385

Db 342 ST-----AGAGATGCI-----IGGIINAIL 361

RESULT 6

A44194

poliovirus receptor (clone AGM-alpha-1) - green monkey

C/Species: Cercopithecus aethiops (green monkey, grivet)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C/Accession: A44194

R/Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotch, O.; Nomoto, A.

J. Virol. 66, 7059-7066, 1992

A/Title: A second gene for the African green monkey poliovirus receptor that has no put

A/Reference number: A44194; PMID:93059651; PMID:1331508

A/Accession: A44194

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-417 <KOI>

A/Cross-references: GB:S48777

C/Superfamily: poliovirus receptor; immunoglobulin homology

C/Keywords: transmembrane protein

F/259-314/Domain: immunoglobulin homology <IMM>

Query Match 10.7%; Score 244; DB 2; Length 417;

Best Local Similarity 23.5%; Pred. No. 7.2e-10;

Matches 108; Conservative 70; Mismatches 192; Indels 90; Gaps 18;

Qy 13 AAAAAAAPPGLRLTLILFSAALIPDQGNLFTKDYTV--IEGEVATISC--QYNK 68

Db 2 ARTMAAAMP-----LTLTLELSMPPGGDIIVQAPVQVPGHLSVTLPCVLQVPG 55

Qy 69 SDDSVIQLNPR-----QTIYFDRFLKDSRFOLNFSSEELKVLTVNS-----I 116

Db 56 MEETHSQLTWSRHGESSMAVFNQTOGPNYSEPRLEFVAARLGTLELDASLRMFGRLV 115

Qy 117 SDEGRYFCQLYTDPQESVYT---ITVLVPPRNLMIDIQDXTAVEGEIEV--NCTAMASK 172

Db 116 EDEGNYTC-LVTFPQGSRSYDINRVLAKQN-TAVQK-VOLGKRVPARCVSTGSR 172

Qy 173 PATTTRMKNGTELKSGKEVEE---WSDYTVTSQMLKVKHEDDGVPLIQVHEPVA 228

Db 173 PPAHTTW---HSDLGGMNTEQAPGLSGTIVTISLWLVSSQVDGKSVCKVHESESFE 229

Qy 229 GNLQTRYLEVQYKPOVHIQMTYPLQGLTREGDALETCENIGKPOVMTVWVRVDEMP 288

Db 230 KQOLITVNLTYIYPEVIS-GYDNNWYLSONEA-TLTCDAARSNEPFGYMWSTTMGRLP 287

Qy 289 GHAVLISGPNLFINNLNTDNGTCRCASNIIVGKAHSDYMLVYDPTTTPPTTTTTTTT 348

Db 288 PRAVAQGAQOLLRPYDKRINTTFICNVTNALGAQAEVTVQKGPSPSPGMSN--- 343

Qy 349 TTTTTLITLITDSRAGEGSIKAVDAVIGGVAVVAFMLCLITL-----GYFAHK 403

Db 344 -----ITLILIGVILLTLTIGIVFYRSR 369

Qy 404 GT-----YFTHAKGADPAADDTIINABGQNNSEKKE 439

Db 370 CSREFLMCHLSPSEEHASA-----SANGYISYSDVGRE 404

RESULT 7

HLMSF3

poliovirus receptor homolog precursor - mouse
 C:Species: Mus musculus domesticus (western European house mouse)
 C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
 C:Accession: A38211
 R:Morison, M.E.; Racanelli, V.R.
 J. Virol. 66, 2807-2813, 1992
 A>Title: Molecular cloning and expression of a murine homolog of the human poliovirus re
 A:Reference number: A38211, MUID:92219365, PMID:1560525
 A:Accession: A38211
 A:Molecule type: DNA
 A:Residues: 1-467 <MOR>
 A:Cross-references: GB:M80206; NID:g19785; PIDN:AAA9734.1; PID:g199786
 C:Superfamily: poliovirus receptor; immunoglobulin homology
 C:Keywords: duplication; glycoprotein; transmembrane protein
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-467/Product: poliovirus receptor homolog #status predicted <MAT>
 F:26-334/Domain: extracellular #status predicted <EXT>
 F:47-133/Domain: immunoglobulin homology <IMM1>
 F:167-231/Domain: immunoglobulin homology <IMM2>
 F:267-322/Domain: immunoglobulin homology <IMM3>
 F:355-374/Domain: transmembrane #status predicted <TMN>
 F:375-467/Domain: intracellular #status predicted <INT>
 F:54-131,174-229,274-320/Dissulfide bonds: #status predicted
 F:128,138,315/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 10.7%; Score 244; DB 1; Length 467;
 Best Local Similarity 21.0%; Pred. No. 8.3e-10;
 Matches 101; Conservative 74; Mismatches 201; Indels 104; Gaps 16;

15 AAAAAAPG-----LRLRLLLLSAALIPFGDGNLFTKQVTEGEV---ATISQV 66
 2 ARAAVLPFSLSLTLPPLLL-----LLETGADVAVRVLPVGRGLGTVBPCPL 56
 QY 67 -----NKSDSVYQLNPNRCIYFRDPKDSRFQV-----INFSS 105
 DB 57 LPTTERVSGVTVQRDLDTVAAFHPS-----FGVDPSNQSFGKRLSFVARPEINADLR 112
 QY 106 ELKVSILTVSISDEGRYFQQLYTD--PQESYTTIVLVPPRLMIDICKDTAVGESE 163
 DB 113 DATLAFRGRLVEDEGNTCEFAFPNGTRGVTLVLAQPE-----HARQEV 163
 QY 164 V-----NCTMASKPATTIRWPKG--NTELKGESEVEMDMYVTSQMLKYHKED 214
 DB 164 IGGQSAVAVACVSTGGRPARITWISSLGEADQEPGLQAGTITIIIRYSLVVGARD 223
 QY 215 GVPYICQVEHPAVTGNLQTORLYEVQKQVHIQMTYPLQGLTRBGDALELTCEAIGK 274
 DB 224 GVKVTCGEHESEFEPEILLPVTLSVRYPPVSVIS--GYDNWVLYGRSEAI--LTQDVRSNPE 281
 QY 275 PAVWTVWRVDEMPQHAIVLSPMLFINLNKKTNGTYRCEASNVIGKASDMLVYVDP 334
 DB 282 PTIYDMSTISGVFPASNAQSQLLVHSDKMNNTFTITATNAVGTGAEGVILVDP 341
 QY 335 TIRPPTTTTTTTTTTTTTLITIDSRAGEGSGIRAVDHAIVGVAVVFA--MLCL 392
 DB 342 QA-----SR-----DVGPLVWAGVGLTLLVLLAAGFLAI 372
 QY 393 IILGRYFAHKGTYFTHKAGADA-----ADAPTAIINAEQGNNSSEKKE 439
 DB 373 LILGRRRRKSPGGGAGDGRGYDPTQVFGNGGPFVFRSASBPBRPDRGDEDEEBE 432

RESULT 8
 JE0099
 neutral cell adhesion molecule 1 - African clawed frog
 N:Alternate names: N-CAM 1
 C:Species: Xenopus laevis (African clawed frog)
 C>Date: 19-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
 C:Accession: JE0099
 R:Kudo, M.; Takayama, E.; Tadokuma, T.; Shiokawa, K.
 Biochem. Biophys. Res. Commun. 245, 127-132, 1998
 A>Title: Molecular cloning of ssd-form neutral cell adhesion molecules (N-Cams) as the ma
 A:Reference number: JE0099; MUID:96204770; PMID:9535795

A:Accession: JE0099
 A:Molecule type: mRNA
 A:Residues: 1-725 <KID>
 A:Cross-references: DDBJ:AB008162; NID:g3116226; PIDN:BA25531.1; PID:g3116227
 A:Experimental source: heart
 C:Comment: This protein mediates and regulates various cell-cell interactions through bo
 C:Superfamily: neutral cell adhesion molecule; fibronectin type III repeat homology; immu
 F:413-475/Domain: immunoglobulin homology <IMM>
 F:512-589/Domain: fibronectin type III repeat homology <3R>

Query Match 10.6%; Score 243; DB 2; Length 725;
 Best Local Similarity 26.5%; Pred. No. 1.7e-09;
 Matches 90; Conservative 61; Mismatches 147; Indels 42; Gaps 15;

50 KDVTIVEGEVATISC---QVN---KSDSVYQLN-----PNRQTIYFRDPKDSRFQ 99
 DB 199 KDQIVTVWPTTIOARLRNATAKMAESVYLSGADGFPDPIISMLKKEPIEDE-EX 257
 QY 100 INFSSSLKVSILTVSISDEGRYFQQLYTD--PQESYTTIVLVPPRLMIDICKDTAV 159
 DB 258 ISFNEQSEMTIHVEKQDEAEVSC--IANNQAEALITLKYARPKTIYENKTAHEL 316
 QY 160 EEIENCTAMASKPATIRW-----FKGNTLKGSEVEEMDMYVTSQMLKYHKE 212
 DB 317 DEITLTCEA--SGDPIETTRAVRINSSAATLIDGHIYKHIIR-----SALTLDIQ 371
 QY 213 DDGVVTCQVEHPAVTGNLQTORLYEVQKQVHIQMTYPLQGLTRBGDALELTCEAIGK 272
 DB 372 TDAGEYFCIASNP--IGVDMQAM--YFEVQYAPKIR-----GVVVYTWEGNPNVITCEVFAH 425
 QY 273 PQPMTWTVAVDDEMPH-----AVLSGP---MLFINLNKKTNGTYRCEASNVIGKAS 324
 DB 426 PR-AAVTWFRDQGLPESNSNIKIYSGPSSLEVPDSENDPGNINCTAIWITIGHS 484
 QY 325 DYMLVYVDPPTIIPPTTTTTTTTTTTTTLITIDSRAG 364
 DB 485 EFLVQADTPSS---PAIRKVEPYSSVLMVPEPDPSTGG 521

RESULT 9
 168093
 PRR2 delta - human
 C:Species: Homo sapiens (man)
 C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000
 C:Accession: 168093
 R:Berle, F.; Dubreuil, P.; Mattei, M.G.; Devillard, E.; Lopez, M.
 Gene 159, 267-272, 1995
 A>Title: The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is ch
 A:Reference number: 153960; MUID:95347610; PMID:7622062
 A:Accession: 168093
 A:Status: preliminary; translated from GB/EWBL/DD84
 A:Molecule type: mRNA
 A:Residues: 1-538 <RES>
 A:Cross-references: GB:S79172; NID:g1042204; PID:g1042205
 C:Genetics:
 C:Superfamily: poliovirus receptor; immunoglobulin homology
 F:276-331/Domain: immunoglobulin homology <IMM>

Query Match 10.6%; Score 242.5; DB 2; Length 538;
 Best Local Similarity 22.6%; Pred. No. 1.3e-09;
 Matches 111; Conservative 66; Mismatches 202; Indels 113; Gaps 17;

10 SOCAAAAAAPGLRLRLLLLSAALIPFGDGNLFTKQVTEGEVATISCQVNS 69
 DB 2 ARAAALPSPSPPLMLPPLLL-----LLETG--AQDVRYQVLPVVG-----QLGCT 49
 QY 70 DDSVYQLNP-----NQTIVFRDPRFKDSRF-----QLNFS 104
 DB 50 VELPCHLLPVPGLYISLVWQRPDAPAHQNV--AAFHKQKPSPPSPGGERISFVS 107
 QY 105 S-----ELKVSILTVSISDEGRYFQQLYTD--PQESYTTIVLVPPRLIMI 149

Db	372	TDEGEFYCIASNF-IIVDQAM-YEVQYAKPIR----	GPVVVYTWEGNPINICEVFAH	423
Qy	273	POEVMYTWVRVDDEMOH-----AVLSGG--	NLEPINLITDNGYRCEASNIYGAHS	324
		: : : : : : : : : : : : : : : :	: : : : : : : : : : : : : : :	
Db	426	PR-AATWTFEDQGLSSNFSNIKIYSGTSSLELVN	DSNDGNYCTAINTIGHFS	484
Qy	325	DYMLUYVDPETIPPTTTTTTTTTTTTTLLI	IDSAG	364
		: : : : : : : : : : : : : : :	: : : : : : : : : : : : : :	
Db	485	EFILVQADTPSS---PAIKRVEPSTWIVDEEDSG	521	

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 7, 2004, 05:56:13 ; Search time 29.126 Seconds

(without alignments)
790.187 Million cell updates/sec

Title: US-10-622-237-2
Perfect score: 2283

Sequence: 1 MASVILPSGSGCAAAAAA.....ATINAGGQNNSEKEYFI 442

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	266.5	11.7	515	1 PVR1_PIG	099176 homo scrofa
2	256.5	11.2	517	1 PVR1_HUMAN	015223 mus scrofa
3	247.5	10.8	530	1 PVR2_MOUSE	P32807 mus musculus
4	244	10.7	417	1 PVR2_CERAP	P32806 cercoptidac
5	242.5	10.6	538	1 PVR2_HUMAN	Q92892 homo sapien
6	240	10.5	417	1 PVR1_HUMAN	P15151 homo sapien
7	239	10.5	515	1 PVR1_MOUSE	Q91456 mus musculus
8	239	10.5	1088	1 NCAL_XENLA	P16170 xenopus lae
9	231	10.1	344	1 NTR1_MOUSE	Q99510 mus musculus
10	230	10.1	344	1 NTR1_PAT	Q62718 ratu
11	228	10.0	344	1 NTR1_HUMAN	Q99121 homo sapien
12	223.5	9.8	837	1 NCW2_MOUSE	O35136 mus musculus
13	223	9.8	1092	1 NCW2_XENLA	P36335 xenopus lae
14	222	9.7	837	1 NCW2_HUMAN	O15394 homo sapien
15	222	9.7	1242	1 NPHN_MOUSE	Q98892 mus musculus
16	219	9.6	337	1 OPCW_CHICK	Q98892 gallus gall
17	218.5	9.6	345	1 OPCW_BOVIN	P11834 bos taurus
18	217.5	9.5	583	1 C166_MOUSE	Q61490 mus musculus
19	217	9.5	588	1 C166_CHICK	P42292 gallus gall
20	216.5	9.5	345	1 OPCW_HUMAN	Q14982 homo sapien
21	213.5	9.4	4391	1 PGBW_HUMAN	P98160 homo sapien
22	210.5	9.2	345	1 OPCW_RAT	P32736 ratu
23	209	9.2	338	1 LAMP_HUMAN	Q98919 gallus gall
24	209	9.2	353	1 CEPY_CHICK	Q90773 gallus gall
25	208	9.1	1493	1 NBO1_MOUSE	P97798 mus musculus
26	207	9.1	847	1 CD22_HUMAN	P20273 homo sapien
27	206.5	9.0	1331	1 CTA2_HUMAN	Q91066 homo sapien
28	206	9.0	702	1 CEAS_HUMAN	P06731 homo sapien
29	205.5	9.0	338	1 LAMP_HUMAN	Q13449 homo sapien
30	205.5	9.0	509	1 SHS1_PAT	P97710 r
31	205.5	9.0	646	1 MUI8_HUMAN	P43121 homo sapien
32	205.5	9.0	1461	1 NBO1_HUMAN	Q92855 homo sapien
33	204	8.9	3707	1 PGBW_MOUSE	Q05793 mus musculus

ALIGNMENTS

RESULT 1	ID	PVR1_PIG	STANDARD	PRT	515 AA
AC	099176				
DT	16-OCT-2001	(Rel. 40, Created)			
DT	16-OCT-2001	(Rel. 40, Last sequence update)			
DT	10-OCT-2003	(Rel. 42, Last annotation update)			
DE	Poliiovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (Hvrc) (Nectin 1).				
DE	PVR1 OR PVR1 OR HVRC.				
OS	Sus scrofa (Pig).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.				
OX	NCBI_TaxID=9623;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	MEDLINE=21176378; PubMed=11277703;				
RA	Milne R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J., Cohen G.H.,				
RT	"Porcine Hvrc, a member of the highly conserved Hvrc/nectin 1 family, is a functional alphaherpesvirus receptor."				
RL	Virology 281:315-328(2001).				
CC	- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO CELLS.				
CC	- SUBUNIT: Interacts with HSV glycoprotein D (gD) (By similarity).				
CC	- SUBCELLULAR LOCATION: Type I membrane protein.				
CC	- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.				
CC	- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.				
CC	- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
CC	EMBL; AF308632; AAC30281.1; -				
DR	HSSP; P06907; INEU				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003596; Ig_v.				
DR	Pfam; PF00047; Ig_2.				
DR	SMART; SMO0406; IGV; 1.				
DR	ProSITE; PS50835; IG_LIKE; 2.				
KW	Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane; Repeat; Glycoprotein; Signal.				
FT	SIGNAL	1	30		POTENTIAL.
FT	CHAIN	31	515		POLIOVIRUS RECEPTOR RELATED PROTEIN 1.
FT	DOMAIN	31	355		EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	356	376		POTENTIAL.
FT	DOMAIN	377	515		CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	31	141		IG-LIKE V-TYPE.
FT	DOMAIN	145	243		IG-LIKE C2-TYPE 1.
FT	DOMAIN	247	334		IG-LIKE C2-TYPE 2.
FT	DOMAIN	437	443		POLY-GLU.

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FT DOMAIN 444 447 POLY-GLY
FT DISULFID 51 124 BY SIMILARITY.
FT DISULFID 172 226 BY SIMILARITY.
FT DISULFID 269 316 BY SIMILARITY.
FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 286 286 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 307 307 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 515 AA; 57047 MW; BFA00320DDE3785 CRC64;

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Query Match 11.7%; Score 266.5; DB 1; Length 515;
Best Local Similarity 24.8%; Pred. No. 9e-12;
Matches 108; Conservative 63; Mismatches 163; Indels 101; Gaps 18;

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QY 52 VTVEEVAATISQVAKSDSVTLQNLNPNROTIFRPPRLKDSRFOLINPSSSELYSL 111
DB 62 ITQVTWQKATNGSKQK-----VAIYNPAMGVSVLAPYR-----ERVEFLRPSFTDGTIRL 111
QY 112 TNVSISEDEGRYPCQLYTDP--QESYTTITVLVPPNLMIDQ-----KDTAVEGEE 161
DB 112 SRLTEDEGVITCEFAFPAGNRESQNLTVMAKPTNMEGTQAVLRAGKGDYV--- 167
QY 162 IEVNTAASAKPATITRFKNTLKGSEVEE--SDMTVTSQMLKVKHEDGVPV 218
DB 168 IVALTCSANGKPSVSW---ERHLKGEAYOEINPNQTVVISRYRLVPEREDHQS 224
QY 219 TCOVEHPAVTGNLTQRY-----LEVQYEPQVHIQ---NTYVLOGLTREGALTECAI 270
DB 225 ACTV-----NYHMDRFRESITLNVQYEPVITIEFDGNWYLOMD-----VKLTQCAD 272
QY 271 GKPQPMVTWVRVDMPHVAVLGSEPLINN-LNKTDNGRCASNTVGAHSDYMLY 329
DB 273 ANPAPHEVMTLNGSLPKGVANQNTLFFRGPINYSAGTYICANTNPIGRSQVBN 332
QY 330 VDPPTTTPPTTTTTTTTTTTTTTTTTTTTTITSDRAGEEGSIRAVNAVIGVVA--VVVF 386
DB 333 ITFPTPTSPPE-----HGRRAQ-----VPAITIGGVGSILVLF 369
QY 387 AMCLIIIGRYPARHKGTYFT-----HEAKG-----DDAADADYAI 424
DB 370 VVGIVVALCRRHHTKGYSTKHYNGCYKAGIPQHHPVAQNLQYPEDSDDEKKA- 428
QY 425 INAEGQNNSEKKE 439
DB 429 -GPIGSSYEHEEE 442

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RESULT 2
PVR1_HUMAN STANDARD; PRT; 517 AA.
ID PVR1_HUMAN Q15223; O75465; O9HB6; O9HBW2;
AC Q15223; O75465; O9HB6; O9HBW2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Poliovirus receptor related protein 1 precursor (Herpes virus entry
DE mediator C) (Hec) (Nectin 1) (Herpesvirus Ig-like receptor) (HIGR)
DE (CD11 antigen).
GN PVR1 OR PRR1 OR HVEC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBITaxid=9606;
RN 1)
RP SEQUENCE FROM N.A. (ISOFORM DELTA).
RX MEDLINE=95237621; PubMed=7721102;
RA Lopez M., Eberle F., Mattei M.-G., Gabert J., Bardin F., Maroc C.,
RA Dubreuil P.;
RT "CDNA characterization and chromosomal localization of a gene related
RT to the poliovirus receptor gene.";

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RL Gene 155:261-265 (1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM DELTA).
RX MEDLINE=98279152; PubMed=9616127;
RA Geraghty R.J., Krumenacher C., Cohen G.H., Eisenberg R.J.,
RA Spear P.G.;
RT "Entry of alphaherpesviruses mediated by poliovirus receptor-related
RT protein 1 and poliovirus receptor.";
RL Science 280:1618-1620 (1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM GAMMA).
RX MEDLINE=21256041; PubMed=11356977;
RA Lopez M., Cocchi F., Avitabile B., Leclerc A., Adelaide J.,
RA Campadelli-Fiume G., Dubreuil P.;
RT "Novel, soluble isoform of the herpes simplex virus (HSV) receptor
RT nectin (or prr1-HIGR-Hvec) modulates positively and negatively
RT susceptibility to HSV infection.";
RL J. Virol. 75:5684-5691 (2001).
RN [4]
RP SEQUENCE OF 28-517 FROM N.A. (ISOFORMS ALPHA AND DELTA), AND DISEASE.
RX MEDLINE=20392396; PubMed=10932188;
RA Suzuki K., Hu D., Bustos T., Zlotogora J., Richieri-Costa A.,
RA Helms J.A., Spritz R.A.;
RT "Mutations of PVR1L, encoding a cell-cell adhesion
RT molecule/herpesvirus receptor, in cleft lip/palate-ectodermal
RT dysplasia.";
RL Nat. Genet. 25:427-430 (2000).
CC -1- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR
CC ALPHAHERPESTIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO
CC CELLS.
CC -1- SUBUNIT: Interacts with HSV glycoprotein D (gD).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms alpha and
CC delta). Secreted (isoform gamma).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=Delta;
CC IsoId=Q15223-1; Sequence=Displayed;
CC Name=Alpha;
CC IsoId=Q15223-2; Sequence=VSP_002626; VSP_002627;
CC Name=Gamma;
CC IsoId=Q15223-3; Sequence=VSP_002624; VSP_002625;
CC -1- DISBASE: Defects in PVR1L are a cause of cleft lip/palate-
CC ectodermal dysplasia syndrome (CLPED1) [MIM:225000]. CLPED1 is
CC responsible for allelic forms known as Margarita island ectodermal
CC dysplasia [MIM:225060] and Zlotogora-Oguz syndrome.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -1- DATABASE: NAME=PROV; NOTE=PROV 2:45-49 (2001);
CC WWW="http://www.ncbi.nlm.nih.gov/prov/guide/2005693930.g.htm".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL, X76400; CA53980.2; ALT_INIT.
DR EMBL, AF060231; AAC23798.1; -.
DR EMBL, AY029539; AAK3124.1; -.
DR EMBL, AF252867; AAG16648.1; -.
DR EMBL, AF196768; AAG16648.1; JOINED.
DR EMBL, AF196769; AAG16648.1; JOINED.
DR EMBL, AF196770; AAG16648.1; JOINED.
DR EMBL, AF196771; AAG16648.1; JOINED.
DR EMBL, AF196774; AAG16649.1; -.
DR EMBL, AF196768; AAG16649.1; JOINED.
DR EMBL, AF196769; AAG16649.1; JOINED.
DR EMBL, AF196770; AAG16649.1; JOINED.
DR EMBL, AF196771; AAG16649.1; JOINED.
DR EMBL, AF196772; AAG16649.1; JOINED.
DR EMBL, AF196773; AAG16649.1; JOINED.

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DR Genew: HGNC:9706; PVRL1.
DR MIM: 600644; -.
DR MIM: 225000; -.
DR GO: GO:0016021; C: integral to membrane; NAS.
DR GO: GO:0004895; F: cell adhesion receptor activity; NAS.
DR GO: GO:0015026; F: coreceptor activity; TAS.
DR GO: GO:0006955; P: immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_2.
DR SMART: SM00406; IgV_1.
DR PROSITE: PS00835; IG_Like_2.
KM Cell adhesion: Immunoglobulin domain; Receptor; Transmembrane;
KM Repeat; Glycoprotein; Signal; Alternative splicing.
FT CHAIN 1 30
FT SIGNAL 1 30
FT CHAIN 31 517
FT DOMAIN 31 355
FT TRANSMEM 356 376
FT DOMAIN 377 517
FT DOMAIN 31 141
FT DOMAIN 149 238
FT DOMAIN 247 334
FT DOMAIN 437 444
FT DOMAIN 445 449
FT DISULFID 51 124
FT DISULFID 172 226
FT DISULFID 269 316
FT CARBOHYD 36 72
FT CARBOHYD 72 139
FT CARBOHYD 139 202
FT CARBOHYD 202 286
FT CARBOHYD 286 297
FT CARBOHYD 307 307
FT CARBOHYD 332 332
FT CARBOHYD 332 352
FT VARSPLIC 353 517
FT VARSPLIC 336 458
FT VARSPLIC 459 517
FT SEQUENCE 517 AA; 57158 MW; DF34CBAEC893EBSD CRC64;
Query Match 11.2%; Score 256.5; DB 1; Length 517;
Best Local Similarity 25.5%; Pred. No. 4.7e-11;
Matches 105; Conservative 60; Mismatches 154; Indels 93; Gaps 19;
QY 74 IQLNPNKQTYFPDPRFKLSRPOLNFSSESLKSLTNVSIIDDERGYCQLYTPDP-- 131
DB 78 VAIYFSPKGVSVLAPYR---ERVEFLRPFSTDTQIRLSRLLEDEGVYCEFTFPTGN 133
QY 132 QESTTITVLPVPRNLMIDIQD--TAVGEIEV---NCTMASKPATTTIRWFGNTELK 187
DB 134 RESQNLTVMAKPTWIGTQAVYRAKKGGQDQKLVATCISANKPSPSVSM---ETRLK 190
QY 188 GKSEVEEN---SDMYTTSQMLKXHKEDDGVYICQVEHPAVTGNLTQORY-----LEV 239
DB 191 GEAEYOEIRNPNNGVTIVISRYRLVPSREAHQOOSLACTV-----NYHMDFKESLTINV 243
QY 240 QYKPPVNHQ---MRYPLQGLTRREGDALHLCGAKPPQVWTVWVYVDDEMPCHAVLSGP 296
DB 244 QIEPEVITIEGPDGNVYLQRMQD-----VLTCKADANPAPATRYHTTLNGSLPKVEAQR 298
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QY 297 NLPTNN-LNKTDNGTYRCEASNIWKAHSDMYLVYDPTTIPPTTTTTTTTTTIL 355
DB 299 TLFFKGPINVSIACTYICGATNPIGTRSGQVEVITFEPTSPHPE----- 344
QY 356 TIITDSRAGEBSIRANDHAVIGVAVVYFAMCLIIIGRYA-----RH--KGYET- 408
DB 345 ---HGRAG-----PVPYALIGVAGST---LVLIVAGGIYVALRRRHTTFKGYDSTK 392
QY 409 -----HEAKGA-----DDAADTATINAGGONNSEKKE 439
DB 393 KHYVNGSKAGKIPQHHPMAQNQYRDDSDDEKKA--GFLGGSSYEESSE 442
RESULT 3
PVR2_MOUSE STANDARD; PRT; 530 AA.
ID P32507.062096;
AC 01-OCT-1993 (Rel. 27, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Poliovirus receptor related protein 2 precursor (Murine herpesvirus
DE entry protein B) (Hvrb) (Nectin 2) (Poliovirus receptor homolog).
GN PVR2 OR PVS OR PVR OR MPH.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
(1)
SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=92219365; PubMed=1560525;
RT Morrison M.E., Racanietello V.R.;
RT "Molecular cloning and expression of a murine homolog of the human
RT poliovirus receptor gene";
RL J. Virol. 66:2807-2813 (1992).
(2)
SEQUENCE FROM N.A. (ISOFORM BETA).
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=94179228; PubMed=8132569;
RT Aoki J., Koike S., Ise I., Sato-Yoshida Y., Nomoto A.;
RT "Amino acid residues on human poliovirus receptor involved in
RT interaction with poliovirus";
RL J. Biol. Chem. 269:8431-8438 (1994).
(3)
SEQUENCE FROM N.A. (ISOFORM BETA).
RP STRAIN=FVB/N; TISSUE=Colon;
RC MEDLINE=22388257; PubMed=12477932;
RX Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Martusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.C., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKernan K.D., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley A.W., Touchman J.W., Green E.D., Myers R.M.,
RA Rodriguez R.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
(4)
CHARACTERIZATION.
RP MEDLINE=99214397; PubMed=10196354;
RX Shukla D., Rowe C.L., Dong Y., Racanietello V.R., Spear P.G.;
RT "The murine homolog (Mph) of human herpesvirus entry protein B (Hvrb)
RT mediates entry of pseudorabies virus but not herpes simplex virus
RT types 1 and 2.";
```

```

OY 106 ELKASVLNWSISSEGGYFQOLVTD--POESYTIITVLVPPRNLMIDIQCDTAVEBEE 163
DB 113 DATLARGLRAVEDBEGYTCFEATFPNGRGVTLMRVIAQDEN-----HAEKQSVT 163
OY 164 V-----NCTAMASKPATITRMFKG-NTELKKKSEVEWSDMYTIVTQMLKFAKEDD 214
DB 164 IGFQSAVARCSTGGRPPARITWISSLGGCAKXDTQEPFGIAGVTIIISRYSLVPGRAD 223
OY 215 GVGVICGVHHPAVTNGLQCRATLEFYQYKQVQHICMTFPLQGLRREGDALELTCEALGKQ 274
DB 224 GVAVTTRVHSEBEEPIILPTLVLSVRYPEVIS-GYDQNMVYIGRSBAL-LTCDVRSNPE 281
OY 275 PVMWTVWRVDEMPQHAVALSGENPFINLNTLTDGTGRCAASNIYVKAHSDYMLVYDDP 334
DB 282 PTDYDKSTTSGVFASAVAGSQGLVHSDVMWNTFTCTATNAVGTRAGQVILVRES 341
OY 335 TTPPTPTTTTTTTTTTTLITLITDSAGSEGSIRAVDAVYIGGVAVVY 385
DB 342 ST-----AGAGATGGI-----IGGIIMAIT 361

RESULT 4
PVR CERAE
ID _PVR CERAE STANDARD; PRT: 417 AA.
AC P32506;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Poliovirus receptor precursor.
PVR OR PVS.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Bkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
OC Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
OC Cercopithecinae, Cercopithecus.
OX NCBI_TaxId=9534;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND DELTA).
RC TISSUE=Kidney.
RX MEDLINE=93059651, PubMed=1331508;
RA Koike S., Ise I., Sato Y., Yonekawa H., Gotoh O., Nomoto A.;
RT "A second gene for the African green monkey poliovirus receptor that
RT has no putative N-glycosylation site in the functional N-terminal
RT immunoglobulin-like domain."
RT J. Virol. 66:7059-7066(1992)."
RL
CC -!- FUNCTION: Not known. Used by poliovirus to bind and enter the
CC cell.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform alpha).
CC Secreted (isoforms beta and gamma).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=Alpha;
CC IsoId=P32506-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=P32506-3; Sequence=Not described;
CC Name=Gamma;
CC IsoId=P32506-4; Sequence=Not described;
CC Name=Delta;
CC IsoId=P32506-2; Sequence=VSP 002622, VSP 002623;
CC -!- SIMILARITY: Contains 1 immunoglobulin-like Y-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -----
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CC -----
DR EMBL, D12611; BA020136.1; -
DR EMBL, D12612; BA020137.1; -
PIR; A44194; A44194.

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DR PIR; B44194; B44194.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig_3.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS00835; IG_LIKE; 3.
 KM Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; signal;
 KM Repeat; Alternative splicing.
 FT SIGNAL 1 20
 FT CHAIN 21 417
 FT DOMAIN 21 343
 FT TRANSMEM 344 367
 FT DOMAIN 368 417
 FT DOMAIN 24 139
 FT DOMAIN 145 237
 FT DOMAIN 244 328
 FT DISULFID 49 123
 FT DISULFID 166 221
 FT DISULFID 266 312
 FT CARBOHYD 85 85
 FT CARBOHYD 120 120
 FT CARBOHYD 188 188
 FT CARBOHYD 237 237
 FT CARBOHYD 278 278
 FT CARBOHYD 307 307
 FT CARBOHYD 313 313
 FT VARSPLIC 386 392
 FT VARSPLIC 393 417
 SQ SEQUENCE 417 AA; 45464 MW; DA4AD0FE4DF6B1F CRC64;
 Query Match 10.7%; Score 244; DB 1; Length 417;
 Best Local Similarity 23.5%; Pred. No. 2.8e-10;
 Matches 108; Conservative 70; Mismatches 192; Indels 90; Gaps 18;

13 AAAAAAPGRLRLILFLSAALIPDQGNLTQKVTY--IGEVATISC--QVAK 68
 2 ARMTAAAMP-----LLTLLELSMPPETGDIIVQAPVQVGFAGDSVTLPCYIQVG 55
 69 SDDSVIQLNPNR-----CTVFRDRPLKDSRFQNLNFSSEELKVSILTVS-----I 116
 56 MEETHVSQLTWSSHGSGMAVHQGPNVSEPKRLIEFVAARLTGLRDASLRPFGLRY 115
 117 SDGRVYCCQIYTPDPQSYTT---ITLVPRRLMDIDQDTAVBGESEIV--NCTAMAK 172
 116 EDEGNVYC-LFVTFPGGSRSDVIMRLVLAEPN-TAEVOK-VQLTGKPVFVARCVSTGR 172
 173 PATTIRFKANTELKSEVEE-----WSDMYVTLSQMLKVHKEDGVPTCCVHPAVT 228
 173 PPAHITM---HSDLGMPNLSQAPGLSGIVTYSIMLVPSQVQVGSKTVCVHESE 229
 229 GNIOTORYLEVQKQVHIQMTYPLQGLTRGDALBELTCAIKPQFVMTVTRVDEMP 288
 230 KPQLLVNLTIVYVPEVISI-GYDNMYLISQNEA-ILTCARSNPEPTGYNSTWGPP 287
 289 QHAYLGPENLFINNNTDNGTVRCASNTVKGASNYMLVYVDPPTTPPTTTT 348
 288 PFAVQAQQLIRVDPKPIITTFICVNTNALGARQALITYQVDEGPSSSGSSN----- 343
 349 TTTTTLITTTDSRAGEGSIKAVDAVAGVAVVAVFAMCLILIL---GRYPAHK 403
 344 -----IIIFLLIGIVILITLLIGIVYFGRSR 369
 404 GT-----YFTHAKGADDAADADATIALNAEGGNSEKKE 439
 370 CSREFLWCHILSPSESEHSA-----SANGYISIVSRE 404

RESULT 5
 FVR2_HUMAN STANDARD; PRT; 538 AA.
 ID_PVR2_HUMAN
 AC_Q92692; O75455; Q96J29;

DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Poliovirus receptor related protein 2 precursor (Herpes virus entry
 DE mediator B) (HvEB) (Nectin 2) (CD112 antigen).
 GN PVR2 OR PRR2 OR HVES.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NCBI_Taxid=9606;
 [1]
 RP SEQUENCE FROM N.A. (ISOFORM DELTA).
 RX MEDLINE=95347610; PubMed=7622062;
 RA Eberle F., Dubreuil P., Mattei M.-G., Devillard E., Lopez M.;
 RT "The human PRR2 gene, related to the human poliovirus receptor gene
 (PVR), is the true homolog of the murine MPB gene.";
 RL Gene 159:267-272(1995).
 [2]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RX MEDLINE=95321161; PubMed=9657005;
 RA Warner M.S., Geraghty R.J., Martinez W.M., Montgomery R.I.,
 RA Whitebeck J.C., Xu R., Eisenberg R.J., Cohen G.H., Spear P.G.;
 RT "A cell surface protein with herpesvirus entry activity (HvEB) confers
 RT susceptibility to infection by mutants of herpes simplex virus type
 RT 1, herpes simplex virus type 2, and pseudorabies virus.";
 RL Virology 246:179-189(1998).
 [3]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RC TISSUE=Brain;
 RX MEDLINE=22386257; PubMed=12477932;
 RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Stausberg R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhac N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brancston M., Soares M.B., Bonaldi M.F., Casavant T.B., Scheetz T.E.,
 RA Stampslein M.J., Usdin T.B., Toshiyuki S., Carrinetti P., Prange C.,
 RA Raba S.S., Iaconello N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Boeck S.A., McEwan P.C., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Holyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.W., Maira M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [4]
 RP SEQUENCE OF 31-538 FROM N.A.
 RA Yoshitake K., Murray J.C.;
 RT "A transcriptional map in the region of 19q13 derived using direct
 RT sequencing and exon trapping.";
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 [5]
 RP SEQUENCE OF 449-538 FROM N.A.
 RX MEDLINE=99449047; PubMed=10520737;
 RA Freitas E.M., Zhang W.J., Lalonde J.P., Tay G.K., Gaudieri S.,
 RA Ashworth L.K., Van Bockmeier F.M., Dawkins R.L.;
 RT "Sequencing of 42kb of the APO E-C2 gene cluster reveals a new gene:
 RT PERC1.";
 RL DNA Seq. 9:89-101(1998).
 CC -I- FUNCTION: RECEPTOR FOR ALPHAHERPESVIRUS (HSV-1, HSV-2 AND
 CC PSEUDORABIES VIRUS) ENTRY INTO CELLS.
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -I- ALTERNATIVE PRODUCTS: Type I membrane protein.
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Delta;
 CC Name=Alpha;
 CC IsoId=C92692-1; Sequence=Displayed;
 CC IsoId=C92692-2; Sequence=vsp_002628, vsp_002629;
 CC

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CC -1- TISSUE SPECIFICITY: Ubiquitous.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.  
CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.  
CC -1- DATABASE: NAME=PROW; NOTE=PROW 1.74-7.7(2000);  
CC WWW="http://www.ncbi.nlm.nih.gov/prov/guide/204270026_g.htm".  
CC  
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CC -----  
DR EMBL; X80038; CAA58342.1; -;  
DR EMBL; AF058448; AAC23797.1; -;  
DR EMBL; BC003091; AAH03091.1; -;  
DR EMBL; AF044968; AAC82348.1; -;  
DR EMBL; AF044962; AAC82348.1; JOINED.  
DR EMBL; AF044963; AAC82348.1; JOINED.  
DR EMBL; AF044964; AAC82348.1; JOINED.  
DR EMBL; AF044966; AAC82348.1; JOINED.  
DR EMBL; AF044967; AAC82348.1; JOINED.  
DR EMBL; AF050154; AAD02503.1; -;  
DR PIR; I68093; I68093.  
DR GENE; HGNC:9707; PVRL2.  
DR MIM; 600798;  
DR GO; GO:0005886; C:plasma membrane; TAS.  
DR GO; GO:0015026; F:coreceptor activity; TAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003599; IG.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SMO0409; IG; 1.  
DR PROSITE; PS50935; IG_LIKE; 3.  
KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;  
KW Repeat; Alternative splicing.  
FT SIGNAL 1 31  
FT CHAIN 32 538  
FT DOMAIN 32 360  
FT TRANSMEM 361 381  
FT DOMAIN 382 538  
FT DOMAIN 32 156  
FT DOMAIN 162 256  
FT DOMAIN 261 345  
FT DISULFID 54 140  
FT DISULFID 183 238  
FT DISULFID 263 329  
FT CARBOHYD 137 137  
FT CARBOHYD 324 324  
FT VARSPPLIC 351 479  
FT FT  
FT FT  
FT FT  
FT FT  
FT FT  
FT FT  
SQ SEQUENCE 538 AA; 57742 MW; 17742 MW; 17742 MW; 17742 MW;  
Query March 10.6%; Score 242.5; DB 1; Length 538;  
Best local similarity 22.6%; Pred. No. 5e-10;  
Matches 111; Conservative 66; Mismatches 202; Indels 113; Gaps 17;  
  
10 SGCACAAAAAPGCRLLRLLLSAALITPTGGQMLFTQDVIVIGEVATISCVNKS 69  
Db 2 ARATAALLPSRPPLLPMLLLL-----LRBTG-AQDVRYVLEAVAG-----QLGCT 49  
70 DDAVYQLLNLP-----NRRTIYFRDPRLPKXSRF-----QLNFSS 104  
50 VELPCHLLPVPGVGLYSILVTWQRDPANHQNV--AAFHPKMGSPFSFKGSERLSFVS 107
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QY	105	S-----	-----ELKVLATVWSISDEGRYFCCLYTDP--	POESYTTITVLVPPRLMI	149
DB	108	AKSGTGDIDAEHLQDNTLALHGLTYVEDGNTCEATIPKKS	VSQGMKMLRVIAKPKV-QA	166	
QY	150	DIDQDPAVEGEELIENVCTIAMASKPATTTIRWFGK-	NTELKGSSEVEWSDMYTVTSQMLMK	208	
DB	167	EAKVWFSSOPTVVALCISKEKRPAPARISWLSISLDMWEAKETQVSGTLAGTATVTSRFTLV		226	
QY	209	VHKEDGVPIQCOVEHPATVGNLQCFQRYLAEVQYKQVACHQMTYPLQGLITREGDALLETCE		268	
DB	227	PSGRADSVYTCVKEVHESFEERALLPVLISRYRPPSVIS-	GYDDNNYLRGTDA-TLSCD	284	
QY	269	AIKQPOVAVTWVRVDDENPQHAVLSGNPLFINLTKDTNGTYRCEASNIYGRASDYML		328	
DB	285	VRSNPETPGYDMETSGTFPTSAVAQSGQLVIHADSLENTFTVCITVNAVGMGRABQVI		344	
QY	329	VYVDPETTIPPTTTTTTTTTTTTTTILNLIIDSRAEGEGSI	RAVDHAVIGVAVVVFPM	388	
DB	345	FVRETFNT-----	AGAGATGT-----IGGIITAAITATA	373	
QY	389	LCILLILIGRYPAHKQTYFTFEHAKGADDAAD-----	TAIIINAE-----G	429	
DB	374	VANTGILLICRQQRKEQT-----	LQGAEDDEDLGGPPSYKPTPRAXKLEAQEMSQLFTLG	428	
QY	430	GQNNSEKXEYF	441		
DB	429	ASEHSEPLKTPYF	440		

RESULT 6

ID	PYR_HUMAN	STANDARD;	PRT;	417 AA.
AC	P15151; P15152; Q15267; Q15268;			
DT	01-APR-1990 (Rel. 14, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Poliiovirus receptor precursor (CD155 antigen).			
GN	PVR OR PYS.			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxId=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
EX	MEDLINE=89168426; PubMed=2538245;			
RA	Mendelsohn C.L., Wimmer E., Racomello V.R.;			
RT	"Cellular receptor for poliiovirus: molecular cloning, nucleotide			
RT	sequence, and expression of a new member of the immunoglobulin			
RT	superfamily.";			
RL	Cell 56:855-865 (1989).			
RN	[2]			
RP	REVISIONS.			
RA	Racomello V.R.;			
RL	Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.			
EX	MEDLINE=91060015; PubMed=2170108;			
RA	Koike S., Horie H., Ise I., Okitsu A., Yoshida M., Iizuka N.,			
RA	Takeuchi K., Takegami T., Nomoto A.;			
RT	"The poliiovirus receptor protein is produced both as membrane-bound			
RT	and secreted forms.";			
RL	EMBO J. 9:3217-3224 (1990).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Kodoyianni V., Severin J., Ge Y., Grable L., Kvistad E., Gordon L.,			
RA	Shannon M., Brower A., Olsen A.S., Smith L.M.;			
RT	"Sequence analysis of a 1Mb region in 19q13.2 containing a zinc finger			
RT	gene cluster.";			
RL	Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	DOMAINS.			
EX	MEDLINE=91239515; PubMed=18511992;			
RA	Koike S., Ise I., Nomoto A.;			

RT "Functional domains of the poliovirus receptor";
Proc. Natl. Acad. Sci. U.S.A. 88:4104-4108(1991).
RN [6]
RX MUTAGENESIS OF CARBOHYDRATE-LINKAGE SITES.
RA MEDLINE=93059689; PubMed=1331527;
RT Zibert A., Wimmer E.,
RT "N glycosylation of the virus binding domain is not essential for
function of the human poliovirus receptor";
J. Virol. 66:7368-7373(1992).
CC -1- FUNCTION: Not known. Used by poliovirus to bind and enter the
cell.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms alpha and
delta). Secreted (isoforms beta and gamma).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=Alpha
CC IsoId=PI151-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=PI151-2; Sequence=VSP_002617;
CC Name=Gamma;
CC IsoId=PI151-3; Sequence=VSP_002618, VSP_002619;
CC Name=Delta;
CC IsoId=PI151-4; Sequence=VSP_002620, VSP_002621;
CC MISCELLANEOUS: THE V-TYPE DOMAIN IS NECESSARY AND SUFFICIENT FOR
VIRUS BINDING AND UPTAKE.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -1- DATABASE: NAME=PROV; NOTE=CD guide CD155 entry;
WWW=http://www.ncbi.nlm.nih.gov/prov/cd/cd155.htm".
CC -----
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CC -----
DR EMBL; M24407; AAA36461.1; -;
DR EMBL; M24406; AAA36462.1; -;
DR EMBL; X64116; CAA45478.1; -;
DR EMBL; X64117; CAA45478.1; JOINED.
DR EMBL; X64118; CAA45478.1; JOINED.
DR EMBL; X64119; CAA45478.1; JOINED.
DR EMBL; X64120; CAA45478.1; JOINED.
DR EMBL; X64121; CAA45478.1; JOINED.
DR EMBL; X64122; CAA45478.1; JOINED.
DR EMBL; X64123; CAA45478.1; JOINED.
DR EMBL; X64116; CAA45479.1; -;
DR EMBL; X64117; CAA45479.1; JOINED.
DR EMBL; X64118; CAA45479.1; JOINED.
DR EMBL; X64119; CAA45479.1; JOINED.
DR EMBL; X64120; CAA45479.1; JOINED.
DR EMBL; X64121; CAA45479.1; JOINED.
DR EMBL; X64122; CAA45479.1; JOINED.
DR EMBL; X64123; CAA45479.1; JOINED.
DR EMBL; X64116; CAA45480.1; JOINED.
DR EMBL; X64117; CAA45480.1; JOINED.
DR EMBL; X64118; CAA45480.1; JOINED.
DR EMBL; X64119; CAA45480.1; JOINED.
DR EMBL; X64120; CAA45480.1; JOINED.
DR EMBL; X64121; CAA45480.1; JOINED.
DR EMBL; X64122; CAA45480.1; JOINED.
DR EMBL; X64123; CAA45480.1; JOINED.
DR EMBL; AC068948; AAE69803.1; -;
DR PIR; A43024; RMH0P.
DR PIR; S12048; RMH0P.
DR GENE; HGNC:9705; PVR.
DR MIM; 173850; -;
DR GO; GO:0005737; C:cytoplasm; TAS.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0007125; P:invasive growth; TAS.

DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS00835; Ig_LIKE_3.
KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
Repeat; Antigen; Alternative splicing; Polymorphism.
FT SIGNAL 1 20
FT CHAIN 21 417
FT DOMAIN 21 343
FT TRANSMEM 344 367
FT DOMAIN 368 417
FT DOMAIN 24 139
FT DOMAIN 145 237
FT DOMAIN 244 328
FT DISULFID 49 123
FT DISULFID 166 221
FT DISULFID 266 312
FT CARBOHYD 105 105
FT CARBOHYD 120 120
FT CARBOHYD 188 188
FT CARBOHYD 218 218
FT CARBOHYD 237 237
FT CARBOHYD 278 278
FT CARBOHYD 307 313
FT CARBOHYD 313 313
FT VARSPLIC 340 384
FT VARSPLIC 331 331
FT VARSPLIC 332 384
FT VARSPLIC 385 392
FT VARSPLIC 393 417
FT VARSPLIC 67 67
FT VARIANT 340 340
FT VARIANT 417 AA; 45302 KM; D15C01CE8531698 CRC64;
SQ SEQUENCE 417 AA; 45302 KM; D15C01CE8531698 CRC64;
Query Match 10.5%; Score 240; DB 1; Length 417;
Best Local Similarity 25.9%; Pred. No. 5.5e-10;
Matches 107; Conservative 53; Mismatches 177; Indels 76; Gaps 17;
QY 14 AAAAAAPPGLRLRLLLLFSAALLPTGGGONLFTKDYV-----IEGEVATISQ 65
2 AAAAAAPPGLRLRLLLLFSAALLPTGGGONLFTKDYV-----IEGEVATISQ 50
QY 66 V---NKSDSVYQL---NPNRQTIYPRDFPLKDSRFOLLNFSSELSKSLTNVNS--- 115
51 LQVPMNETHYSQLMWAKHSGSMAVHQOQPGSYSSKLEFPAALGALRLRASLRM 110
QY 116 ----SDSGRYFCQLYTDPQESYTT---ITVLPNRMIMIDIQCTAVGESEIV-NCT 167
111 FGLRVEDBGNVTC-LFTVFPQGRSDVIDLRLVLAKPON-TAEVQR-VOLTEPVMARCV 167
QY 168 AAKSKPATIRFKKNTLKGSEVEW-SDVATYTSQMLKVKHEDDGVPIYCOVEHPA 226
168 STGGRPPAQITWHSDLGKPNTSQVPGFISGVATYISLWILVPSQVDSKNTCAVEHES 227
QY 227 VTGNLQTCRYLEVQYKPOVHIQMTYPLQGLTREGDABELTCAIGKPOVWTVVRVDE 286
228 FEKRPQLITNLTVVYVPEVIS-GYDNWVYLGQNEA-LTLCARASNPEPTGYMSTWGP 285
QY 287 MPQHAVLSGPNFPINNKAKTDNGYRCASNVVGAHSDMYLYVDDPTTTPPTTTTT 346
286 LPFPAVAGACOLLIRVDKPIINTTILCNVTNLAGRQBELTVQVEGSPS----- 335
QY 347 TTTTTLTITDSRAGEGSIKRAVDHVGVAVAVFAMLCILITIGRYF 399
336 -----EHSGISR-NALIFLVGILVF---LTLIGIYF 365

FT	DOMAIN	31	354	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	355	375	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	376	515	IG-LIKE V-TYPE.
FT	DOMAIN	31	141	IG-LIKE C2-TYPE 1.
FT	DOMAIN	145	243	IG-LIKE C2-TYPE 2.
FT	DOMAIN	247	334	POLY-GLY.
FT	DOMAIN	436	442	POLY-GLY.
FT	DOMAIN	443	447	POLY-GLY.
FT	DISULFID	51	124	BY SIMILARITY.
FT	DISULFID	172	226	BY SIMILARITY.
FT	DISULFID	289	316	BY SIMILARITY.
FT	CARBOHYD	36	36	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	72	72	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	139	139	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	202	202	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	286	286	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	297	297	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	332	332	N-LINKED (GLCNAC. . .)
FT	CONFLICT	138	138	L -> P (IN REF. 1).
FT	CONFLICT	165	165	N -> D (IN REF. 1).
FT	CONFLICT	342	342	P -> P (IN REF. 2).
FT	CONFLICT	428	428	S -> G (IN REF. 3).
SEQ	SEQUENCE	515 AA:	57064 MM:	FF608BEBF7BA0F CRC64;

Query Match 10.5%; Score 239; DB 1; Length 515;
Best Local Similarity 24.4%; Pred. No. 8.5e-10;
Matches 98; Conservative 59; Mismatches 142; Indels 102; Gaps 18

Qy	91	PLKDSRFLNLFSSSELKVSILNNVISDEGEYFQCLYDPP--QESYTIIVLVPPRYLM	148
Db	91	PPEKRVAFELPSPFDGTRILSGLEDEGMYICEFATPTGNRSQNLTVMAKPTW-	149
Qy	149	IDICKDTAV---EGEEIEV--NCTAMASRPATTIRFKNTLKGKSEVEW---SDM	198
Db	150	--IGSTAVLAKRGQDNKVLVACTSANGKRPASV---ETRLKGEAEVGEIRNPGT	204
Qy	199	YTVTSQMLKXHKEDDGVPIYCOVEHPAVTNLQTOR---LEVQYKPOY-----	245
Db	205	VTVISRYALVPSRAHRSQSLACIV-----NYHLDERRESLTLNVQYEPETIEGPDGN	257
Qy	246	-HIQWTVPLQGLTREBDALETGCAIGKPGQVMTWVRVDEDMOHAVLSGPNLFINN-L	303
Db	258	WYLQRT-----DVKLTCADANPAPTEVHTWTLNLSLPGKVAQNRITLFFRPDI	306
Qy	304	NKTDNGTYRCASNVIGKASHSDYMLVYVDPPTIIPPTTTTTTTTTTILLITDSRA	363
Db	307	TYSLAGTYVICBATNPIGRSGQVEVNITEPPYT-PTPE-----HGRRRA	348
Qy	364	GEESSIAVDHAVIGGVAVVVFAMLC---LLIILGTYFAHKGTYPT-----	408
Db	349	GQ-----MPTAIIIGVAGSVLLVLIVVGGIIVALLRRRRHTEFKDYSTKXVNGYSKA	402
Qy	409	---HEAKGA-----DDAADADATAIINAEGGNSSSEKKE	439
Db	403	GIPQHHPMAQNQLYPPDSDDEKKA--SLPGSSSYEEEEE	441

RESULT 8
NCAL XENLA STANDARD; PRT; 1088 AA.
AC PL6170;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Neutral cell adhesion molecule 1, 180 kDa isoform precursor (N-CAM DE 180)
DE NCAM1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xeropodinae; Xenopus.
NC NCB1_TaxID=8355;
LN [1]

[illegible]

FT	CARBOHYD	472	472	M-LINKED (GLCNAC...)	(POTENTIAL)
FT	VARSPLIC	804	1049	Missing (in isoform N-CAM 140).	
FT				/FTID=VSP_002589.	
SO	SEQUENCE	1088 AA,	11778 MM,	62738B5B03F3E83 CRC64,	
	Query Match	10.5%,	Score 239;	DB 1;	Length 1088;
	Best Local Similarity	26.2%,	Pred. No. 2.2e-09;		
	Matches	89;	Conservative	62;	Mismatches 147; Indels 42; Gaps 15
OY	50	KDVTVIEGEVATISCG---QVWKS---DDSVYQLIN---	PKRQTTIRFDFFPLDPSRQL	95	
DB	199	KDIDIVVNVPPETIQARQLRVATNMAEVSVLSCDADGFPDPPELSWLRKGPBIDEG-EK	257		
OY	100	LNPFSSSELKVLTVNWSISDEGRYFCOLYTDPEQESYTTITVLVPPRNLIMIDIKDTAVEG	159		
DB	258	ISFNEDESEMTIHHEVDEKDEHVEYSC-IANNAGAEALETILLKAYAKPITVYENKTAHEL	316		
OY	160	EEIEVNCTAMASKPATITRW-----FKGNTELKGSVEEWSMDYTVISQLMKYKE	212		
DB	317	DEILTLTCEA-SGDPIPSITWRTAVRNISSEATITLDGHIVKEHIRM-----SALTLDKIDQY	371		
OY	213	DDGVFVLCQVHEHPVATGNLQFORLVEYQKQVCHQWTVPLQSG-LTREGDALELTGEAIGK	272		
DB	372	TDAGEFYCLISNP-IQVDMQM-YFEQYAPKIR---GPIVYVTTWBNPNNITCEVPAH	425		
OY	273	PQPMVWTVWVRVDDMPQH-----AVLSGF---NLFINLNKTNDGTGRCEASNTVGRKAS	324		
DB	426	PR-AAATWFRDQGLPSSNFENIKIYSGPTSSLEVPDSENDPCGNVCTAINTIGHEFS	484		
OY	325	DYMLVYVDPPTTTPPTTTTITTTTITTTITTTITTTITTTITTTITTTITTTITTTITTTITTT	364		
DB	485	EFILVQADTPBS---PAIRKVEPYSSVTWIVFDEPDSGCG	521		
RESULT 9					
ID	NTRI_MOUSE	STANDARD;	PRT;	344 AA.	
AC	Q99PJ0;				
DT	28-FEB-2003	(Rel. 41, Created)			
DT	28-FEB-2003	(Rel. 41, Last sequence update)			
DT	10-OCT-2003	(Rel. 42, Last annotation update)			
DE	Neurotrophin precursor.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_Taxid=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=ICR; TISSUE=Brain;				
RA	Kim T.H., Choi S.C., Kim J., Jeon J.W., Kim K.D., Lee S.H.;				
RT	"Cloning and expression of mouse neurotrophin gene in the developing				
RL	nervous system."				
RL	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6; TISSUE=Eye;				
PX	MEDLINE=22388257; PubMed=12479932;				
RA	Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Batow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Ditchen L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stadlen W., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,				
RA	Rata S.S., Loquellano N.A., Peters G.J., Adamson R.D., Mullany S.J.,				
RA	Bosak S.A., McGowan P.U., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Foley J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,				
RA	Butterfield J.S.N., Krzywinski M.T., Skalska V., Smalhus D.E.,				

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- FUNCTION: Neural cell adhesion molecule.
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily. IgLON
 CC family.
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC
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 CC
 CC EMBL: AF282987; AAK0276.1; -
 CC EMBL: BC023307; AAK23307.1; -
 CC InterPro: IPR007110; Ig-like.
 CC InterPro: IPR003599; Ig.
 CC InterPro: IPR003598; Ig_c2.
 CC Pfam: PF00047; Ig; 3.
 CC SMART: SM00409; Ig; 3.
 CC SMART: SM00408; IgC2; 3.
 CC PROSITE: PSS0835; IG_Like; 3.
 DR Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
 KM Repeat; Signal; Lipoprotein.
 FT CHAIN 1
 FT PROPEP 32 321
 FT DOMAIN 32 344
 FT DOMAIN 39 126
 FT DOMAIN 136 218
 FT DOMAIN 222 309
 FT DISULFID 57 115
 FT DISULFID 157 201
 FT CARBOHYD 243 295
 FT CARBOHYD 44 44
 FT CARBOHYD 70 70
 FT CARBOHYD 152 152
 FT CARBOHYD 284 284
 FT CARBOHYD 292 292
 FT CARBOHYD 305 305
 FT CARBOHYD 321 321
 FT LIPID 321
 FT CONFLICT 75 75
 FT CONFLICT 92 92
 FT CONFLICT 119 119
 FT CONFLICT 187 187
 FT CONFLICT 213 213
 FT CONFLICT 225 225
 SQ SEQUENCE 344 AA; 37984 MW; C885BBA52C148554 CRC64;
 Query Match 10.1%; Score 231; DB 1; Length 344;
 Best Local Similarity 26.2%; Pred. No. 1.9e-09;
 Matches 84; Conservative 54; Mismatches 136; Indels 46; Gaps 14;
 QY 29 LILLFAAALITPGDONLFTK---DVTVEGVATISQVKKSDSVIOLNPNRQTI- 84
 DB 19 LRLFLVPGVPRSGDATPKAMDNVTRQGSATLRCTI---DNRVTRVAMLRSTLL 75
 QY 85 YFDFPPLKDSRQOLNFSSELKSLVLSIVNSISDEGRYCOLYTD-PROESTTTITLVLP 143
 DB 76 YANDRWKCLDPRVLLSNITQYSIEICNVADVDESPYCSVQTDNHPKTSRVHLIVQVS 135
 QY 144 PRLMLTDIQKDTAV-EGEELEVNTAMAKSPATTIMFKGNTELGKSKSVEEWSMNYVT 202
 DB 136 PK--IYEISDISINQNNISITCIA-TGRPEPTVWRIRISPKAVGFSVSEDIYELIGGIT 192
 QY 203 SOLMLKVA--KEDDVPIYCYEHPAVTGNLTQOTRYLEYQYKPOVHIOMTYPILOGL-TR 258

DB 193 REQGEYECASNDVAAPVRRYK-----VTVNPPIYS-----EAKGTGP 234
 QY 259 EGDALLETCEAIGKPPQVMTVWRVDEMPQ-----HAVLGPNLEFINNKTDG 309
 DB 235 VGQKGTIGCEASAAPS-AEFQWFPDRRLVEGKGVVENRPLSKLTFF--NVSEHDVG 291
 QY 310 TYRCEASNTYKXASDITMLY 329
 DB 292 NYTCVANSKLGHTVASIMLF 311
 RESULT 10
 NRRL RAT
 ID NRRL RAT STANDARD; PRT; 344 AA.
 AC Q62718;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Neurotrophin precursor (Gp65).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 217-229.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=95198094; Pubmed=7891157;
 RA Struyk A.F., Canoll P.D., Wolfgang M.J., Rosen C.L., D'Eustachio P.,
 RA Salzer J.L.;
 RT "Cloning of neurotrophin defines a new subfamily of differentially
 RT expressed neural cell adhesion molecules";
 RL J. Neurosci. 15:2141-2156(1995).
 CC -1- FUNCTION: Neural cell adhesion molecule.
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -1- TISSUE SPECIFICITY: Central nervous system.
 CC -1- DEVELOPMENTAL STAGE: Expressed at high levels in several
 CC developing projection systems: in neurons of the thalamus,
 CC subplate, and lower cortical laminae in the forebrain and in the
 CC pontine nucleus, cerebellar granule cells, and Purkinje cells in
 CC the hindbrain.
 CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily. IgLON
 CC family.
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: U16845; AAK67445.1; -
 CC PIR: I56551; I56551.
 CC InterPro: IPR007110; Ig-like.
 CC InterPro: IPR003598; Ig_c2.
 CC Pfam: PF00047; Ig; 3.
 CC SMART: SM00409; Ig; 3.
 CC PROSITE: PSS0835; IG_Like; 3.
 KW Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
 KM Repeat; Signal; Lipoprotein.
 FT CHAIN 1
 FT PROPEP 32 321
 FT DOMAIN 32 344
 FT DOMAIN 39 126
 FT DOMAIN 136 218
 FT DOMAIN 222 309
 FT DISULFID 57 115
 FT DISULFID 157 201
 FT DISULFID 243 295
 FT CARBOHYD 44 44
 FT CARBOHYD 70 70
 FT CARBOHYD 152 152

```
FT CARBOHYD 216 216 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 284 284 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 305 305 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 321 321 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 321 321 GPI-anchor amidated asparagine
FT LipID 321 321 (Potential).
SQ SEQUENCE 344 AA; 37998 MW; CBB3BEB3B3B24 CRC64;

Query Match 10.1%; Score 230; DB 1; Length 344;
Best Local Similarity 26.2%; Pred. No. 2.2e-09;
Matches 84; Conservative 53; Mismatches 137; Indels 46; Gaps 14;

Qy 29 LLLLSAALIPFGDGNLFTR---DVTVEGEVATISQVKNKSDSVIQLNPNQGT- 84
Db LRLFLVPTGVPRSGATFPKAMDNVTRQGESATLACTI---DNKRVAMLNRSITL 75
85 YFRDFRPLKDSRFQNLNFSSEELKSLTVNSISDEGRFCQLYTD-PPQESYTTITVLP 143
76 YAGNDKMCILDPKRVVLNSTQTOYSIEIQNVVYDEGPTCSQTDNHPKTSRVHLIVQS 135
Qy 144 PNLMTIDIOKDTAV-EGEEIEVNCVTAMASKPATITRFKNTLEKSKSEVEESDMYVT 202
Db 136 PK--IVEISSDISINEGNNISLTCTA-TGRPEPTVTRHISPKAVGVSEDEYLEIOGIT 192
Qy 203 SOLMLKVH---KEDDGVPIQCVHEPVAVTGNLCTORYLEVQYKPCVHIQMTYPLQGL-TR 258
Db 193 REGSGEYECASANDVAAPVVRV-----VTNYPYIS-----EAKGTVP 234
Qy 259 EGDALLETCEALGKQPVMTVTRVDEMPQ-----HAVLSGENFINLNKTDNG 309
Db 235 VGQKGTLOCEASAVPS-AEFQWFKDDKRLVEGKGVKVENRPLSLRTPF--NVSEHDYG 291
Qy 310 TYRCEASNIYKASHDYMLY 329
Db 292 NYTCVANSKLGHTNASIMLF 311

RESULT 11
NTRI HUMAN STANDARD; PRT; 344 AA.
AC OPR121;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neurotrophin precursor (hnt).
GN NT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
ON NCBI_TaxID=9606;
RX [1]
RP SEQUENCE FROM N.A.
RA Li G., Jin X., Tan X., Hu S., Yuan J., Qiang B.;
RT "Cloning and identification of human neurotrophin full length cDNA.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Neural cell adhesion molecule.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily. IgION
CC family.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -----
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CC or send an email to license@ebi.ac.uk).
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DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00408; IgC2; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
KW Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
KW Repeat; Signal; Lipoprotein.
FT SIGNAL 1 31
FT CHAIN 32 321
FT PROPEP 322 344
FT DOMAIN 39 126
FT DOMAIN 136 218
FT DOMAIN 222 309
FT DISULFID 57 115
FT DISULFID 157 201
FT DISULFID 243 295
FT CARBOHYD 44 44
FT CARBOHYD 70 70
FT CARBOHYD 152 152
FT CARBOHYD 284 284
FT CARBOHYD 292 292
FT CARBOHYD 305 305
FT CARBOHYD 321 321
FT LipID 321 321
SQ SEQUENCE 344 AA; 37971 MW; DA4D12C295ABBE3A CRC64;

Query Match 10.0%; Score 228; DB 1; Length 344;
Best Local Similarity 26.4%; Pred. No. 3.1e-09;
Matches 84; Conservative 54; Mismatches 138; Indels 42; Gaps 14;

Qy 29 LLLLSAALIPFGDGNLFTR---DVTVEGEVATISQVKNKSDSVIQLNPNQGT- 84
Db LRLFLVPTGVPRSGATFPKAMDNVTRQGESATLACTI---DNKRVAMLNRSITL 75
85 YFRDFRPLKDSRFQNLNFSSEELKSLTVNSISDEGRFCQLYTD-PPQESYTTITVLP 143
76 YAGNDKMCILDPKRVVLNSTQTOYSIEIQNVVYDEGPTCSQTDNHPKTSRVHLIVQS 135
Qy 144 PNLMTIDIOKDTAV-EGEEIEVNCVTAMASKPATITRFKNTLEKSKSEVEESDMYVT 202
Db 136 PK--IVEISSDISINEGNNISLTCTA-TGRPEPTVTRHISPKAVGVSEDEYLEIOGIT 192
Qy 203 SOLMLKVH---KEDDGVPIQCVHEPVAVTGNLCTORYLEVQYKPCVHIQMTYPLQGL-TR 258
Db 193 REGSGEYECASANDVAAPVVRV-----VTNYPYIS-----EAKGTVP 234
Qy 259 EGDALLETCEALGKQPVMTVTRVDEMPQ-----AVLSGP---NLFINLNKTDNGTY 311
Db 235 VGQKGTLOCEASAVPS-AEFQWFKDDKRLVEGKGVKVENRPLSLRTPF--NVSEHDYG 293
Qy 312 RCEASNIYKASHDYMLY 329
Db 294 TCVASNKLGHTNASIMLF 311

RESULT 12
NCM2 MOUSE STANDARD; PRT; 837 AA.
AC O35136; O35962;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neural cell adhesion molecule 2 precursor (N-CAM 2) (RB-8 neural cell
DE adhesion molecule) (F4B12).
GN NCM2 OR OCAM OR RNCAM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RX [1]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RC STRAIN=BALB/c; TISSUE=Olfactory neuroepithelium;
```

FT	CARBOHYD	406	406	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	419	419	N-LINKED (GLCNAC. . .) <th>(POTENTIAL).</th>	(POTENTIAL).
FT	CARBOHYD	445	445	N-LINKED (GLCNAC. . .) <th>(POTENTIAL).</th>	(POTENTIAL).
FT	CARBOHYD	474	474	N-LINKED (GLCNAC. . .) <th>(POTENTIAL).</th>	(POTENTIAL).
FT	CARBOHYD	562	562	N-LINKED (GLCNAC. . .) <th>(POTENTIAL).</th>	(POTENTIAL).
FT	VARSPPLIC	694	837	TFEGGELGAIIGIGVAAALILIVITDVSFFFLRQCGLLNC	ITRMCKSGSGSGSKKEELGEGKAAYAKDGSKEEIVMPTRE
FT				DERITENEDGSPVNEPNETPLPEKEDT,PLKEENGKGLVNA	DEETIKYXNDIIOGSKEDDICA-->NCCENKNGGQGSWH
FT				LNAGVFPIVYTIMSLSCLF (in isoform Short).	
FT				/FtId=VSP_002590.	
SO	SEQUENCE	837 AA;	93203 MW;	70473B053A2D65A5 CRC64;	
	Query Match	9.8%;	Score 223.5;	DB 1;	Length 837;
	Best Local Similarity	27.9%;	Pred. No. 2e-08;		
	Matches	92;	Conservative	52;	Mismatches 111; Indels 75; Gaps 20;
QY	TKDVTVI-----	49	TKDVTVI-----	EGEVAITSCQVNSDSDSVIQLLNDNRQTIYFRDF	89
DB	TOEATVLEIYOKLTFREVVSPGEFKQGEBAEVACRVSSPAPAVSWLYNNEEV-----	102	TOEATVLEIYOKLTFREVVSPGEFKQGEBAEVACRVSSPAPAVSWLYNNEEV-----		155
QY	RPLADSFOLLNFSSSLKTVSLTNVSI SDSGRYFCOLYTPDQE-SYTTITVL--VPPRN	90	RPLADSFOLLNFSSSLKTVSLTNVSI SDSGRYFCOLYTPDQE-SYTTITVL--VPPRN		146
DB	TTIYDNPFAVL-----ANNNIQILINKSDSGIYRCBGRVZARAGEIDPRDITVYNNPPAI	156	TTIYDNPFAVL-----ANNNIQILINKSDSGIYRCBGRVZARAGEIDPRDITVYNNPPAI		211
QY	LTMDIQRD---TAVEGEIEIVNCTAIVASKAPATTIRMFKGNTELKSGSEVMSDMYTV--	147	LTMDIQRD---TAVEGEIEIVNCTAIVASKAPATTIRMFKGNTELKSGSEVMSDMYTV--		201
DB	MM--PQSFNATVATRGSEMTLTCKASGS-PDPTISWPR-----NGKL-IEE-NEKYILKG	212	MM--PQSFNATVATRGSEMTLTCKASGS-PDPTISWPR-----NGKL-IEE-NEKYILKG		261
QY	TSGMLAKVHKEDDGVFVICOVHPHANTGLQTORIYLEVQYKRPQVHIOMTYPLQGLLREG	202	TSGMLAKVHKEDDGVFVICOVHPHANTGLQTORIYLEVQYKRPQVHIOMTYPLQGLLREG		260
DB	SNELTYRNIINKGSGSYCKATNKA--GEDQKQAFLOVHVQPHI-LQLK--NETTSEN	262	SNELTYRNIINKGSGSYCKATNKA--GEDQKQAFLOVHVQPHI-LQLK--NETTSEN		315
QY	DALELTCEAIGKQDPQVATVTVVRV-----DDEMP-----OHAVLSGPNLFINNN	261	DALELTCEAIGKQDPQVATVTVVRV-----DDEMP-----OHAVLSGPNLFINNN		304
DB	GHTVLVEAGAGEPVP-ETTKKALIDGVMEFSGGKSPGRIRLEVKGQHGRRS--LHINDVX	316	GHTVLVEAGAGEPVP-ETTKKALIDGVMEFSGGKSPGRIRLEVKGQHGRRS--LHINDVX		372
QY	KTDNGITTRCE-ASNIYVCKASHSDYMLYYPD	305	KTDNGITTRCE-ASNIYVCKASHSDYMLYYPD		333
DB	LSDSGRYDCEAASRIQGHQSRSMHLIDETAP	372	LSDSGRYDCEAASRIQGHQSRSMHLIDETAP		401
RESULT 13					
NCB2_XENLA					
ID	NCB2_XENLA	STANDARD;	PRT;	1092 AA.	
AC	P36335;				
DT	01-JUN-1994 (Rel. 29, Created)				
DT	01-JUN-1994 (Rel. 29, Last sequence update)				
DT	15-MAR-2004 (Rel. 43, Last annotation update)				
DE	Neural cell adhesion molecule 2, 180 kDa isoform precursor (N-CAM				
DE	180).				
GN	NCAM2.				
OS	Xenopus laevis (African clawed frog).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;				
OC	Xenopodidae; Xenopus.				
OX	NCBI_TaxID=8355;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=93273239; PubMed=7684721;				
RA	Torlissen K.F., Krieg P.A.;				
RT	"Two neural-cell adhesion molecule (NCAM)-encoding genes in Xenopus				
RL	laevis are expressed during development and in adult tissues";				
RL	Gene 127.243.247(1993).				
CC	-!- FUNCTION: This protein is a cell adhesion molecule involved in				
CC	neuron-neuron adhesion, neurite fasciculation, outgrowth of				
CC	neurites, etc.				
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.				
CC	-!- ALTERNATIVE PRODUCTS:				
CC	Event-Alternative splicing: Named isoforms=1;				
CC	Comment=A number of isoforms are produced;				
CC	Name=1;				
CC	IsCID=P36335-1; Sequence=Displayed;				

CC -1- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -----
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 CC -----
 DR EMBL: M76710; AAA4910.1; -.
 DR PIR: JN0635; JN0635.
 DR HSP: P56276; 1TLK.
 DR InterPro: IPR008957; FN_III-like.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003598; IG_c2.
 DR Pfam: PF00041; fn3; 2.
 DR Pfam: PF00047; Ig; 5.
 DR SMART: SM00060; FN3; 2.
 DR SMART: SM00408; IGc2; 4.
 DR PROSITE: PS50835; IG_LIKE; 5.
 DR Cell adhesion; Glycoprotein; Transmembrane; Repeat;
 DR Immunoglobulin domain; Alternative splicing; Signal.
 FT SIGNAL 1
 FT CHAIN 20 1092
 FT
 FT DOMAIN 20 705
 FT TRANSMEM 706 723
 FT DOMAIN 724 1092
 FT DOMAIN 20 108
 FT DOMAIN 113 202
 FT DOMAIN 208 295
 FT DOMAIN 303 397
 FT DOMAIN 400 489
 FT DOMAIN 512 589
 FT DOMAIN 618 686
 FT DOMAIN 149 153
 FT DOMAIN 158 162
 FT DISULFID 41 93
 FT DISULFID 136 186
 FT DISULFID 232 282
 FT DISULFID 323 379
 FT DISULFID 420 473
 FT CARBOHYD 82 473
 FT CARBOHYD 219 219
 FT CARBOHYD 310 310
 FT CARBOHYD 341 341
 FT CARBOHYD 417 417
 FT CARBOHYD 443 443
 FT CARBOHYD 472 472
 SQ SEQUENCE 1092 AA; 118082 MW; CD36B058B7AD1 CRC64;
 Query Match 9.8%; Score 223; DB 1; Length 1092;
 Best Local Similarity 24.2%; Pred. No. 3,1e-08;
 Matches 82; Conservative 67; Mismatches 150; Indels 40; Gaps 15;

QY 274 CPWVTWVRVDDEMPQH-----AVLSGP---NLFINKTNGNGYRCEASNIVKASD 325
 DB 427 S-AASVWRDGLLSSNSFNKIKNGPFPSSLEVPNSPNDPFGNNCSAVNSIGHSSE 485
 QY 326 YMLVYDPEPTTIPPTTTTTTTTTTTTTLTIIDSRAG 364
 DB 486 FIVQADTPSS---PAIRKVEPSTWIVDEPDATG 521
 RESULT 14
 NCAM2 HUMAN
 ID NCAM2 HUMAN STANDARD; PRT; 837 AA.
 AC 015394;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Neural cell adhesion molecule 2 precursor (NCAM 2).
 GN NCAM2 OR NCAM21.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97369930; PubMed=9226371;
 RA Paoloni-Giacchino A., Chen H., Antonarakis S.E.;
 RT "Cloning of a novel human neural cell adhesion molecule gene (NCAM2)
 RT that maps to chromosome region 21q21 and is potentially involved in
 RT Down syndrome";
 RL Genomets 43:43-51(1997).
 RN [2]
 RP CARBOHYDRATE-LINKAGE SITES ASN-445 AND ASN-562.
 RX MEDLINE=22660472; PubMed=12754519;
 RA Zhang H., Li X.-D., Martin D.B., Aebersold R.;
 RT "Identification and quantification of N-linked glycoproteins using
 RT hydroxide chemistry, stable isotope labeling and mass spectrometry";
 RL Nat. Biotechnol. 21:660-666(2003).
 CC -1- FUNCTION: May play important roles in selective fasciculation and
 CC zone-to-zone projection of the primary olfactory axons.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed most strongly in adult and fetal
 CC brain.
 CC -1- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -----
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 CC -----
 DR EMBL: U75330; AAB80803.1; -.
 DR Genew; HGNC:7657; NCAM2.
 DR MIM: 602040; -.
 DR GO: GO:0016021; C:integral to membrane; TAS.
 DR GO: GO:0005886; C:plasma membrane; TAS.
 DR GO: GO:0007158; P:neuronal cell adhesion; TAS.
 DR InterPro: IPR008957; FN_III-like.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003598; IG_c2.
 DR Pfam: PF00041; fn3; 2.
 DR Pfam: PF00047; Ig; 5.
 DR SMART: SM00060; FN3; 2.
 DR SMART: SM00408; IGc2; 5.
 DR PROSITE: PS50835; IG_LIKE; 5.
 DR Cell adhesion; Transmembrane; Glycoprotein; Repeat;
 DR Immunoglobulin domain; Signal.
 FT SIGNAL 1
 FT CHAIN 19
 FT POTENTIAL.

FT CHAIN 20 837 NEURAL CELL ADHESION MOLECULE 2.
 FT DOMAIN 20 697 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 698 718 POTENTIAL.
 FT DOMAIN 719 837 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 837 108 IG-LIKE C2-TYPE 1.
 FT DOMAIN 113 202 IG-LIKE C2-TYPE 2.
 FT DOMAIN 208 297 IG-LIKE C2-TYPE 3.
 FT DOMAIN 302 396 IG-LIKE C2-TYPE 4.
 FT DOMAIN 401 491 IG-LIKE C2-TYPE 5.
 FT DOMAIN 482 581 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 594 678 FIBRONECTIN TYPE-III 2.
 FT DISULFID 42 93 PROBABLE.
 FT DISULFID 136 186 PROBABLE.
 FT DISULFID 232 281 PROBABLE.
 FT DISULFID 322 380 PROBABLE.
 FT DISULFID 422 475 PROBABLE.
 FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 219 219 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 309 309 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 419 419 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 474 474 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 562 562 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 837 AA; 929332 MW; C3D034106C5741C1 CRC64;

Query Match 9.7%; Score 222; DB 1; Length 837;
 Best Local Similarity 24.1%; Pred. No.2.6e-08;
 Matches 120; Conservative 70; Mismatches 172; Indels 136; Gaps 28;

QY 49 TKDVTI-----EGEVATISQVKNSSDSVIGLNPNTQIYFRDF 89
 DB 102 TQKTVVLEIYOKLTFREVVSPQEGEDAEVACVSSPAPAVSMLVHNEEV----- 155
 QY 90 RPLKDSFQOLNSSSLKXSLTNVSTSDGRYFCQLYTDPPE-SYTTITVL--VPERN 146
 DB 156 TTISDNKLAWL-----ANNLQIININSDGIRYCGRYVARGEIDFDITIVAVNPPAI 211
 QY 147 LMDIQKD---TAVEGEIEVNCTAMASKPATIRRFKGNTELKSEVEWSDMYTV-- 201
 DB 212 SM--PQKSPNATLBERGEMTFSCRAGSS-PEPAISWFR-----NGKL-IEE-NEKYLK 261
 QY 202 -TSQMLAKVKKEDDVAVICQVHPAVTGNLQTORLEIYQKQVHIQMTYPLQGLTRBG 260
 DB 262 SNELTYRNINSDGGYVCRATNKA--GEDEKQALQYFVOPHI-IQK---NETTYEN 315
 QY 261 DALELTCEALGKPOPVWTVWR--VD-----DEM-----OHAIVSGENLFTNNLN 304
 DB 316 GQYTLVGDAGEPI-P-EITWKAVDGFTFEGSKSDGRILEVKGQH---GSSSLHKDVX 371
 QY 305 KTDNGYRGE-ASNIYKKAHSDMYLVY-----DPTT 336
 DB 372 LSGSGRYDCBAASRIGCHQKSMYLDIEYAPKFIISNOTIYYSWEGNFINISCDVKNPFA 431
 QY 337 I-----PPTTTTTTTTTTTTTTTTTTTTDSRAGEG--SIRAVDAHVAGVAVAV 385
 DB 432 IHWRRDKLVPAKNTVLTSTGRKVIETAPTSNDGRVCTATN--IGTRQETI 489
 QY 386 FAMLCT-----LIIIGRYPAR-----HKGYTFHAKGADDAADATTAIINAG 429
 DB 490 LALADVSPYGVKIIISQTAQVSNKPSHGVPVHHYQVDAVEASE-IWKIVRSHG 549
 QY 430 GQ-----NNESEKKEYI 442
 DB 550 VQTMVVVNLNDEPNTTYEI 567

RESULT 15
 ID NPIN MOUSE STANDARD; PRT; 1242 AA.
 AC Q50Z57;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)
 GN Nephritin precursor (renal glomerulus-specific cell adhesion receptor).
 CN NPISH OR NPIN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid=10090.
 RN (1)
 RP SEQUENCE FROM N.A., AND SUBCELLULAR LOCATION.
 RX MEDLINE=99436348; PubMed=10504499;
 RA Holzman L.B., St John P.L., Kovari I.A., Verma R., Holtfoefer H.,
 RA Abrahamson D.R.;
 RT "Nephritin localizes to the slit pore of the glomerular epithelial
 RT cell." Int. 56:1481-1491(1999).
 RL Kidney Int. 56:1481-1491(1999).
 RN (2)
 RP INTERACTION WITH CD2AP.
 RX MEDLINE=21590460; PubMed=11733379;
 RA Shih N.Y., Li J., Cotran R., Mundel P., Miner J.H., Shaw A.S.;
 RT "CD2AP localizes to the slit diaphragm and binds to nephrin via a
 RT novel C-terminal domain." J.
 RL Am. J. Pathol. 159:2303-2308(2001).
 RN (3)
 RP INTERACTION WITH CD2AP AND NPISH2.
 RX MEDLINE=21590460; PubMed=11733557;
 RA Schwarz K., Simons M., Reiser J., Saleem M.A., Paul C., Kriz W.,
 RA Shaw A.S., Holzman L.B., Mundel P.;
 RT "Podocin, a raft-associated component of the glomerular slit
 RT diaphragm, interacts with CD2AP and nephrin." J.
 RL J. Clin. Invest. 108:1621-1629(2001).
 CC - FUNCTION: Seems to play a role in the development or function of
 CC the kidney glomerular filtration barrier. May anchor the podocyte
 CC slit diaphragm to the actin cytoskeleton.
 CC - SUBUNIT: Interacts with podocin/NPISH2 and with CD2AP C-terminal
 CC domain.
 CC - SUBCELLULAR LOCATION: Type I membrane protein (potential). Located
 CC at podocyte slit diaphragm between podocyte foot processes.
 CC - TISSUE SPECIFICITY: Expressed in kidney glomeruli.
 CC - PTM: Phosphorylated on tyrosine residues (by similarity).
 CC - SIMILARITY: Belongs to the immunoglobulin superfamily.
 CC - SIMILARITY: Contains 8 immunoglobulin-like domains.
 CC - SIMILARITY: Contains 1 fibronectin type III domain.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF168466; AAF03368.1; .
 CC MGD; MGI:1859637; Nphs1.
 CC GO; GO:0005515; F:protein binding; IPI.
 CC GO; GO:0007254; P:JNK cascade; IDA.
 CC GO; GO:0000165; P:MAPKK cascade; IDA.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF00041; fn3.1.
 DR Pfam; PF00047; Ig.1.
 DR SMART; SM00060; FN3.1.
 DR SMART; SM00408; IGc2.1.
 DR PROSITE; PS00835; IG-LIKE.8.
 KW Cell adhesion; Transmembrane; Signal; Glycoprotein;
 KW Immunoglobulin domain; Repeat; Phosphorylation.
 FT CHAIN 1 22
 FT DOMAIN 23 1242 NEPHRIN.
 FT TRANSMEM 23 1064 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 1087 1086 POTENTIAL.
 FT DOMAIN 1087 1242 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 25 130 IG-LIKE C2-TYPE 1.


```
FT DOMAIN 135 233 IG-LIKE C2-TYPE 2.
FT DOMAIN 242 333 IG-LIKE C2-TYPE 3.
FT DOMAIN 340 434 IG-LIKE C2-TYPE 4.
FT DOMAIN 440 540 IG-LIKE C2-TYPE 5.
FT DOMAIN 544 635 IG-LIKE C2-TYPE 6.
FT DOMAIN 740 832 IG-LIKE C2-TYPE 7.
FT DOMAIN 838 939 IG-LIKE C2-TYPE 8.
FT DOMAIN 941 1025 FIBRONECTIN TYPE-III.
FT DISULFID 53 111 POTENTIAL.
FT DISULFID 160 217 POTENTIAL.
FT DISULFID 265 317 POTENTIAL.
FT DISULFID 361 417 POTENTIAL.
FT DISULFID 465 528 POTENTIAL.
FT DISULFID 567 623 POTENTIAL.
FT DISULFID 761 816 POTENTIAL.
FT DISULFID 863 920 POTENTIAL.
FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 547 547 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 553 553 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 564 564 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 577 577 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 680 680 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 708 708 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 908 908 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1242 AA; 134890 MW; 02D82180BF145092 CRC64;
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Query Match 9.7% Score 222; DB 1; Length 1242;
Best Local Similarity 23.0%; Pred. No. 4,3e-08;

Matches 87; Conservative 74; Mismatches 164; Indels 54; Gaps 16;

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QY 23 GLRLRLLLLSAALIPGSGQN-----LFTKQVYVIEGEVATISQVNSKSD 71
DB 4 GTTRASLL--AGMLTTGAGPVPPTAPRGFWALSENLTVEGSTITKMGV-RAPG 59
QY 72 SVIQ-----LINPQRTIYFRDPRPLKDSRFLNPFSSSELSLTVNSISDEGRYFCQ 125
DB 60 SVVQWADGILLGNPKIPGPPKYSLEGDS-----AKGEFHLLIACDLSDDAEYECQ 112
QY 126 LYTD--PQ--ESYTTITVLPENLMIDIKD---TAVEGEIEVNCNMAASKPATIR 178
DB 113 VGRSELPELVSPRVLISLVPPKVLQTPKAGSTVTWVAGQEVVTCVSGAKPAPDII 172
QY 179 WFKGNTELKG-KSEVEEMSD--MYTVISQMLKYNKEDDGVPIYCOVEHRAVNGNQTQR 235
DB 173 FIOGRTVEDVSSSVNSESSEKLFETAEARVTPQSSDNGQLVCEGSNPAALPIKASF 232
QY 236 YLEVOYKPOVAHQITVP--LOGLTREGDALELTCEAIGKPOPVWTVVVRVDEM-----P 288
DB 233 TMTNLPFPGPPV-IDWGLNMGHVRAGENIELPCIRAGNPPATLQWLKNGKXPVSIAMGT 291
QY 289 QHAVLISGNLFINNLTNDNGT-YRCAASNTVGKASDVMLYVDPPTIIPPTT----- 343
DB 292 EHAQAVASVLMVTRPEDHGARLSCOSYNSVSAETORSITL---CVTRPPSAVITLGS 348
QY 344 TTTTNTTTTTLITITDR 362
DB 349 TSQSENKAVTILCCLTKSSR 367
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Search completed: July 7, 2004, 06:03:53
Job time : 30.126 secs

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OM protein - protein search, using sw model

Run on: July 7, 2004, 05:56:13 ; Search time 61.8289 Seconds

(without alignments)
2255.564 Million cell updates/sec

Title: US-10-622-237-2

Perfect score: 2283
Sequence: 1 MASVVLPSGSGCAAAAAA.....AIINAEQGQNNSEKKEVFI 442

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SPTRMBL_25:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2280	99.9	442	4	Q9BY67
2	2241.5	98.2	445	11	Q8R4L1
3	2232.5	97.8	445	11	Q8K3T6
4	2221	97.3	456	11	Q8S5M8
5	2134.5	93.5	443	4	Q8N2P4
6	2071.5	90.7	417	11	Q7T1L1
7	1715	75.1	333	4	Q86WB8
8	1683.5	73.7	336	11	Q80VG4
9	1671.5	73.2	336	11	Q9DEB7
10	1526	66.8	295	11	Q9Z2H8
11	1503.5	65.9	306	11	Q9QV14
12	1483	65.0	295	11	Q9QV16
13	1394	61.1	289	11	Q9QV15
14	1370.5	60.6	278	11	Q9QV13
15	903	39.6	435	4	Q8N3J6
16	893	39.1	437	4	Q81ZP8

17	863	37.8	395	11	Q8BXJ7	Q8BXJ7 mus musculus
18	862.5	37.8	404	11	Q8BLQ9	Q8BLQ9 mus musculus
19	860	37.7	395	11	Q8BZP4	Q8BZP4 mus musculus
20	858.5	37.6	404	11	Q8BYP1	Q8BYP1 mus musculus
21	802	35.1	394	13	Q7ZXX1	Q7ZXX1 xenopus lae
22	767	33.6	388	4	Q8NFF28	Q8NFF28 homo sapien
23	758	33.2	388	11	Q8R464	Q8R464 mus musculus
24	744.5	32.6	396	11	Q9N2N8	Q9N2N8 mus musculus
25	739	32.4	398	4	Q9N126	Q9N126 homo sapien
26	732.5	32.1	381	4	Q9Y4A4	Q9Y4A4 homo sapien
27	722	31.6	432	4	Q9UUP1	Q9UUP1 homo sapien
28	379.5	16.6	163	11	Q8K1H8	Q8K1H8 mus musculus
29	370.5	16.2	163	4	Q8NVU5	Q8NVU5 homo sapien
30	368.5	16.1	152	11	Q8BSQ8	Q8BSQ8 mus musculus
31	341.5	15.0	549	11	Q9D006	Q9D006 mus musculus
32	338.5	14.8	549	11	Q9JUB9	Q9JUB9 mus musculus
33	335.5	14.7	549	4	Q8NQS3	Q8NQS3 homo sapien
34	325.5	14.3	234	4	Q81Z09	Q81Z09 homo sapien
35	316.5	13.9	438	11	Q9JUB7	Q9JUB7 mus musculus
36	316.5	13.9	510	11	Q9JUB8	Q9JUB8 mus musculus
37	287	12.6	439	13	Q57349	Q57349 gallus gall
38	268	11.7	407	4	Q9Y412	Q9Y412 homo sapien
39	265	11.6	1482	5	Q9V4Y0	Q9V4Y0 drosophila
40	263.5	11.5	5175	5	Q810L3	Q810L3 caenorhabdi
41	263.5	11.5	5198	5	Q76518	Q76518 caenorhabdi
42	261.5	11.5	510	4	Q96NY8	Q96NY8 homo sapien
43	261.5	11.5	510	4	Q96K15	Q96K15 homo sapien
44	254.5	11.1	400	6	Q8HY16	Q8HY16 cebus apell
45	247.5	10.8	530	11	Q80XJ5	Q80XJ5 mus musculus

ALIGNMENTS

RESULT 1

Q9BY67 ID Q9BY67 PRELIMINARY; PRT; 442 AA.
AC Q9BY67;
DT 01-JUN-2001 (TRMBLrel. 17, Created)
DT 01-JUN-2001 (TRMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TRMBLrel. 25, Last annotation update)
DE Necitin-like protein 2.
OS NECD2.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou Y., Du G., Chen J., Yuan J., Qiang B.;
RT "Cloning of a novel human cDNA encoding a member of the immunoglobulin superfamily.";
RT Submitted (Mar-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF132811; AA069029.1; -.
DR GeneW; HGNC:5951; IGSP4.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003585; Neurexin-like.
DR Pfam; PF00047; IG_3.
DR SMART; SM00294; 4.1m; 1.
DR SMART; SM00408; IGc2; 1.
DR PROSITE; PS00835; IG_LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 442 AA; 48537 MW; 68183E3238735062 CRC64;

Query Match 99.9%; Score 2280; DB 4; Length 442;

Best Local Similarity 99.8%; Pred. No. 1.4e-166;

Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASVVLPSGSGCAAAAAAAPPGLRLRLILLIFSAALIFPTGDDQNTFTKQVTVIEGEVA 60
1 MASVVLPSGSGCAAAAAAAPPGLRLRLILLIFSAALIFPTGDDQNTFTKQVTVIEGEVA 60

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QY 61 TISCQVKKSDSDSVIQLNPNRQTIYFRDPRPLKDSRFQNLNFSSELKVSLETVNSISDEG 120
DB 61 TISCQVKKSDSDSVIQLNPNRQTIYFRDPRPLKDSRFQNLNFSSELKVSLETVNSISDEG 120
QY 121 RYFCQLYTDPPOSSEYTTITVLVPPRNLMDIQDRTAVEGEIEVNTCTAMASKPATITIRF 180
DB 121 RYFCQLYTDPPOSSEYTTITVLVPPRNLMDIQDRTAVEGEIEVNTCTAMASKPATITIRF 180
QY 181 KGMTLKGKSEVESEMSDMYTVTSQMLKVHKEDDGVVICOVEHPAVTGNLQTORYLEVQ 240
DB 181 KGMTLKGKSEVESEMSDMYTVTSQMLKVHKEDDGVVICOVEHPAVTGNLQTORYLEVQ 240
QY 241 YKQVHIQMTYPIQGLTRBGDALELTCEAIGKQPPVMTVVRVDDMPQHAVLSGPNLFI 300
DB 241 YKQVHIQMTYPIQGLTRBGDALELTCEAIGKQPPVMTVVRVDDMPQHAVLSGPNLFI 300
QY 301 NNLNKTDNGYRCASNIVGKASHDYM.LVYDPTTIPPTTTTTTTTTTTTTTTTTTTTT 360
DB 301 NNLNKTDNGYRCASNIVGKASHDYM.LVYDPTTIPPTTTTTTTTTTTTTTTTTTTTT 360
QY 361 SRAGEGSIKRAVDHVAIVGVAVVFPMLCLIIIGRYFARHKGYFTHEAKGADDA 420
DB 361 SRAGEGSIKRAVDHVAIVGVAVVFPMLCLIIIGRYFARHKGYFTHEAKGADDA 420
QY 421 DTAIINAEQGNSEKKEYFI 442
DB 421 DTAIINAEQGNSEKKEYFI 442

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RESULT 2

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ID 08R4L1 PRELIMINARY; PRT; 445 AA.
AC 08R4L1;
DT 01-JUN-2002 (TEMBLrel. 21, Created)
DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Tumor suppressor in lung cancer 1.
GN IGSF4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RA Fukami T., Maruyama T., Murakami Y.;
RT "Identification of murine orthologue of the TSL1 gene.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF34663; AL06736.1; -.
DR MGD; MGI:1889272; Igsf4.
DR GO; GO:0045202; C:synaptic junction; IDA.
DR GO; GO:0008021; C:synaptic vesicle; IDA.
DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . .; IDA.
DR GO; GO:0005515; F:protein binding; IPT.
DR GO; GO:0007416; P:synaptogenesis; IDA.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003585; Neurexin-like.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00294; Ig_1m; 1.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 445 AA; 48664 MW; C5DSA070DAF70E55 CRC64;

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Query Match 98.2%; Score 2241.5; DB 11; Length 445;
Best Local Similarity 98.0%; Pred. No. 2.8e-183;
Matches 436; Conservative 1; Mismatches 5; Indels 3; Gaps 1;
QY 1 MASVLPSSGSCAA--AAAAPPGRLRLILLFSAALIFPTGDQNLFTKDVTVIEG 57
DB 1 MASVLPSSGSCAA--AAAAPPGRLRLILLFSAALIFPTGDQNLFTKDVTVIEG 57

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QY 58 EVATISQVKKSDSDSVIQLNPNRQTIYFRDPRPLKDSRFQNLNFSSELKVSLETVNSIS 117
DB 61 EVATISQVKKSDSDSVIQLNPNRQTIYFRDPRPLKDSRFQNLNFSSELKVSLETVNSIS 120
QY 118 DEGRYFCQLYTDPPOSSEYTTITVLVPPRNLMDIQDRTAVEGEIEVNTCTAMASKPATIT 177
DB 121 DEGRYFCQLYTDPPOSSEYTTITVLVPPRNLMDIQDRTAVEGEIEVNTCTAMASKPATIT 180
QY 178 RWFKNTELKGKSEVESEMSDMYTVTSQMLKVHKEDDGVVICOVEHPAVTGNLQTORYL 237
DB 181 RWFKNTELKGKSEVESEMSDMYTVTSQMLKVHKEDDGVVICOVEHPAVTGNLQTORYL 240
QY 238 EVQYKQVHIQMTYPIQGLTRBGDALELTCEAIGKQPPVMTVVRVDDMPQHAVLSGPN 300
DB 241 EVQYKQVHIQMTYPIQGLTRBGDALELTCEAIGKQPPVMTVVRVDDMPQHAVLSGPN 300
QY 298 LFINLNKTDNGYRCASNIVGKASHDYM.LVYDPTTIPPTTTTTTTTTTTTTTTTTTTTT 357
DB 301 LFINLNKTDNGYRCASNIVGKASHDYM.LVYDPTTIPPTTTTTTTTTTTTTTTTTTTTT 360
QY 358 ITDSRAGEGSIKRAVDHVAIVGVAVVFPMLCLIIIGRYFARHKGYFTHEAKGADDA 417
DB 361 ITDSRAGEGSIKRAVDHVAIVGVAVVFPMLCLIIIGRYFARHKGYFTHEAKGADDA 420
QY 418 ADADTATINAEQGNSEKKEYFI 442
DB 421 ADADTATINAEQGNSEKKEYFI 445

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RESULT 3

```

ID 08K3T6 PRELIMINARY; PRT; 445 AA.
AC 08K3T6;
DT 01-OCT-2002 (TEMBLrel. 22, Created)
DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Synaptic cell adhesion molecule 1.
GN IGSF4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL;
RA Biederer T., Sara Y., Mozhayeva M., Atasoy D., Liu X., Kavalali E.T.,
RT "SynCAM, a synaptic adhesion molecule that drives synapse assembly.";
RL Science 0:0-0(2002).
DR EMBL; AF539424; AN01614.1; -.
DR MGD; MGI:1889272; Igsf4.
DR GO; GO:0045202; C:synaptic junction; IDA.
DR GO; GO:0008021; C:synaptic vesicle; IDA.
DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . .; IDA.
DR GO; GO:0005515; F:protein binding; IPT.
DR GO; GO:0007416; P:synaptogenesis; IDA.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003599; IG_c2.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00409; Ig_3.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 445 AA; 5836F23F1877497 CRC64;

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```

Query Match 97.8%; Score 2232.5; DB 11; Length 445;
Best Local Similarity 97.5%; Pred. No. 1.7e-182;
Matches 434; Conservative 2; Mismatches 6; Indels 3; Gaps 1;
QY 1 MASVLPSSGSCAA--AAAAPPGRLRLILLFSAALIFPTGDQNLFTKDVTVIEG 57

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Db 1 MASAVLPSCGSCCAAAAAAAPPGLRLRLLLLLLSAALLIPTGDNLFTRKDVTVIEG 60
QY 58 EVATISCCQVNSDSDSVIQLNPNRQTIYFRDPRPLKDSRFQNLNFSSELKVSILTNVSI 117
Db 61 EVATISCCQVNSDSDSVIQLNPNRQTIYFRDPRPLKDSRFQNLNFSSELKVSILTNVSI 120
QY 118 DEGRYFCQLYTDPPQESYTTITVLPVRNLMIDIOKDTAVEGEIEVNCSTAMSKPATTI 177
Db 121 DEGRYFCQLYTDPPQESYTTITVLPVRNLMIDIOKDTAVEGEIEVNCSTAMSKPATTI 180
QY 178 RWFKGNTELKGSKEVEEWSMDYVTSQMLKVKHEDDGPVICOVEHPATVGNLQTORYL 237
Db 181 RWFKGNTELKGSKEVEEWSMDYVTSQMLKVKHEDDGPVICOVEHPATVGNLQTORYL 240
QY 238 EVOYKPOVHIQMTYPLQGLTREGDALELTCEAIGKPCPVMTVWRVDDENPQHAVLSGPN 297
Db 241 EVOYKPOVHIQMTYPLQGLTREGDALELTCEAIGKPCPVMTVWRVDDENPQHAVLSGPN 300
QY 298 LFINLNKTDNGTYRCEASNIYKASDYMLYYDPTTIPPTTTTTTTTTTTTTTTTTI 357
Db 301 LFINLNKTDNGTYRCEASNIYKASDYMLYYDPTTIPPTTTTTTTTTTTTTTTTTI 360
QY 358 ITTSRAGEGSIKAVDAVAVIGVAVVVFAMLCILITLGRYFARHKGTYTEAKGADA 417
Db 361 ITTSRAGEGSIKAVDAVAVIGVAVVVFAMLCILITLGRYFARHKGTYTEAKGADA 420
QY 418 ADADTALINAEQGNNSSEKKEYFI 442
Db 421 ADADTALINAEQGNNSSEKKEYFI 445

RESULT 4
Q8R5M8 PRELIMINARY; PRT; 456 AA.
ID Q8R5M8;
AC Q8R5M8;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE RA175.
GN IGSF4 OR RA175.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Monol T.;
RT "Biological function of RA175, a new member of immunoglobulin super
RT family."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB064265; BAB83501.2; -.
DR MGD; MGI:1889272; IGSF4.
DR GO; GO:0045202; C:synaptic junction; IDA.
DR GO; GO:0008021; C:synaptic vesicle; IDA.
DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . ; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR GO; GO:0007416; P:synaptogenesis; IDA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003585; Neurixin-like.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00294; 4.1m; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 456 AA; 49787 MW; 32268664B01C7F CRC64;

```

Query Match 97.3%; Score 2221; DB 11; Length 456;
 Best Local Similarity 95.4%; Pred. No. 1,7e-181;
 Matches 435; Conservative 2; Mismatches 5; Indels 14; Gaps 2;

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QY 1 MASVLPSCGSCCAAAA--AAAAAPGLRLRLLLLLLSAALLIPTGDNLFTRKDVTVIEG 57
Db 1 MASAVLPSCGSCCAAAAAAAPPGLRLRLLLLLLSAALLIPTGDNLFTRKDVTVIEG 60
QY 58 EVATISCCQVNSDSDSVIQLNPNRQTIYFRDPRPLKDSRFQNLNFSSELKVSILTNVSI 117
Db 61 EVATISCCQVNSDSDSVIQLNPNRQTIYFRDPRPLKDSRFQNLNFSSELKVSILTNVSI 120
QY 118 DEGRYFCQLYTDPPQESYTTITVLPVRNLMIDIOKDTAVEGEIEVNCSTAMSKPATTI 177
Db 121 DEGRYFCQLYTDPPQESYTTITVLPVRNLMIDIOKDTAVEGEIEVNCSTAMSKPATTI 180
QY 178 RWFKGNTELKGSKEVEEWSMDYVTSQMLKVKHEDDGPVICOVEHPATVGNLQTORYL 237
Db 181 RWFKGNTELKGSKEVEEWSMDYVTSQMLKVKHEDDGPVICOVEHPATVGNLQTORYL 240
QY 238 EVOYKPOVHIQMTYPLQGLTREGDALELTCEAIGKPCPVMTVWRVDDENPQHAVLSGPN 297
Db 241 EVOYKPOVHIQMTYPLQGLTREGDALELTCEAIGKPCPVMTVWRVDDENPQHAVLSGPN 300
QY 298 LFINLNKTDNGTYRCEASNIYKASDYMLYYDPTTIPPTTTTTTTTTTTTTTTTTI 357
Db 301 LFINLNKTDNGTYRCEASNIYKASDYMLYYDPTTIPPTTTTTTTTTTTTTTTTTI 360
QY 358 IT-----DSRAGEGSIKAVDAVAVIGVAVVVFAMLCILITLGRYFARHKGTYTEAKGADA 406
Db 361 ITDTTATTEPRVHDSRAGEGSIKAVDAVAVIGVAVVVFAMLCILITLGRYFARHKGTYTEAKGADA 420
QY 407 FTBEAKGADDAADADTALINAEQGNNSSEKKEYFI 442
Db 421 FTBEAKGADDAADADTALINAEQGNNSSEKKEYFI 456

RESULT 5
Q8N2F4 PRELIMINARY; PRT; 443 AA.
ID Q8N2F4;
AC Q8N2F4;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE RA175.
GN IGSF4 OR RA175.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue=Embryo;
RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
RA Nagahara K., Sugano S., Isogai T.;
RT "HRI human cDNA sequencing project."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK075502; BC01657.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00409; IG_3.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Hypothetical protein; Immunoglobulin domain.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 443 AA; 48648 MW; 046B43A1A56F64 CRC64;

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Query Match 93.5%; Score 2134.5; DB 4; Length 443;
 Best Local Similarity 94.4%; Pred. No. 4.1e-174;
 Matches 418; Conservative 4; Mismatches 20; Indels 1; Gaps 1;

QY 1 MASVLPSCGSCCAAAAAAAPPGLRLRLLLLLLSAALLIPTGDNLFTRKDVTVIEG 60
 Db 1 MASVLPSCGSCCAAAAAAAPPGLRLRLLLLLLSAALLIPTGDNLFTRKDVTVIEG 60
 QY 61 TISQVNSDSDSVIQLNPNRQTIYFRDPRPLKDSRFQNLNFSSELKVSILTNVSI 120

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Db 61 TISQVVKSDSDSVIQLNPNRQTIYFDFRPLKDSRQLNLFSSSELKVLNVS:ISDEG 120
Qy 121 RYFCQLYTDPPOESYTTITVLVPPRNLMDIQKDTAVEGEIEVNCSTAMASKPATIIRMF 180
Db 121 RYFCQLYTDPPOESYTTITVLVPPRNLMDIQKDTAVEGEIEVNCSTAMASKPATIIRMF 180
Qy 181 KGNTELKGSKEVEBWSMNTVTISQLMKVHKEDGVPVICOVHPAVTGNLQTORYLEVO 240
Db 181 KGNTELKGSKEVEBWSMNTVTISQLMKVHKEDGVPVICOVHPAVTGNLQTORYLEVO 240
Qy 241 YKPOVHIQMTYPIQGLTRBGDALELTCEAIGKQPVMVTVVRVDEMPQHAVLSGNLFI 300
Db 241 YKPOVHIQMTYPIQGLTRBGDALELTCEAIGKQPVMVTVVRVDEMPQHAVLSGNLFI 300
Qy 301 NNINKTDNGTYRCEASNIVGKASHDYLVIYDPTTATTEPVRHGLTQLPNSAELEBDESD 360
Db 301 NNINKTDNGTYRCEASNIVGKASHDYLVIYDPTTATTEPVRHGLTQLPNSAELEBDESD 360
Qy 360 DSRAGEGSIKRAVDHAVIGGVAVVVFAMLCILIIIGRYFARHKGTFTHEAKGADDA 419
Db 361 DSRAGEGSIKRAVDHAVIGGVAVVVFAMLCILIIIGRYFARHKGTFTHEAKGADDA 420
Qy 420 ADTALINAEQGQNNSEKKEYFI 442
Db 421 ADTALINAEQGQNNSEKKEYFI 443

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RESULT 6

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ID Q7TNLI PRELIMINARY; PRT; 417 AA.
AC Q7TNLI;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Nectin-like molecule 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Shingai T., Ikeda W., Kakunaga S., Morimoto K., Takekuni K., Itoh S.,
RA Satoh K., Takeuchi M., Imai T., Monden M., Takai Y.;
RT "Implications of nectin-like molecule
RT 2/IGSF4/BA175/SGISF/TSIC1/SYNCAM1 in cell-cell adhesion and
RT transmembrane protein localization in epithelial cells.";
RL J. Biol. Chem 0:0-0(2003).
DR EMBL: AY351388; AA00281.1;
SQ SEQUENCE 417 AA; 45779 MW; 98500180D37845C2 CRC64;

```

Query Match 90.7%; Score 2071.5; DB 11; Length 417;
 Best Local Similarity 91.7%; Pred. No. 9.2e-169;
 Matches 408; Conservative 1; Mismatches 5; Indels 31; Gaps 2;

```

Qy 1 MASVVLPSGSCQCAAA--AAAAAPGRLRLRLLLLSAALLPTGCGQLFTKDVTVIEG 57
Db 1 MASVVLPSGSCQCAAAAVAAAAAPGRLRLRLLLLSAALLPTGCGQLFTKDVTVIEG 60
Qy 58 EVATTICQVVKSDSDSVIQLNPNRQTIYFDFRPLKDSRQLNLFSSSELKVLNVS:IS 117
Db 61 EVATTICQVVKSDSDSVIQLNPNRQTIYFDFRPLKDSRQLNLFSSSELKVLNVS:IS 120
Qy 118 DESGRYFCQLYTDPPOESYTTITVLVPPRNLMDIQKDTAVEGEIEVNCSTAMASKPATI 177
Db 121 DESGRYFCQLYTDPPOESYTTITVLVPPRNLMDIQKDTAVEGEIEVNCSTAMASKPATI 180
Qy 178 RWFKGNTELKGSKEVEBWSMNTVTISQLMKVHKEDGVPVICOVHPAVTGNLQTORYL 237
Db 181 RWFKGNTELKGSKEVEBWSMNTVTISQLMKVHKEDGVPVICOVHPAVTGNLQTORYL 240
Qy 238 EVOYKPOVHIQMTYPIQGLTRBGDALELTCEAIGKQPVMVTVVRVDEMPQHAVLSGN 297

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Db 241 EVOYKPOVHIQMTYPIQGLTRBGDALELTCEAIGKQPVMVTVVRVDEMPQHAVLSGN 300
Qy 298 LPNNLNKTDNGTYRCEASNIVGKASHDYLVIYDPTTATTEPVRHGLTQLPNSAELEBDESD 357
Db 301 LPNNLNKTDNGTYRCEASNIVGKASHDYLVIYDPTTATTEPVRHGLTQLPNSAELEBDESD 357
Qy 358 ITDSRAGEGSIKRAVDHAVIGGVAVVVFAMLCILIIIGRYFARHKGTFTHEAKGADDA 417
Db 355 --DSRAGEGSIKRAVDHAVIGGVAVVVFAMLCILIIIGRYFARHKGTFTHEAKGADDA 392
Qy 418 ADADTALINAEQGQNNSEKKEYFI 442
Db 393 ADADTALINAEQGQNNSEKKEYFI 417

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RESULT 7

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ID Q86WB8 PRELIMINARY; PRT; 333 AA.
AC Q86WB8;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Secretory isoform of TSIC-1.
GN TSIC-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=lung;
RA Ito A., Koma Y., Nagano T.;
RT "Cloning of a secretory isoform of SGISF/TSIC-1."
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB094146; BAC66178.1;
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003598; IG_c2.
DR Pfam: PF00047; IG_3.
DR SMART: SM00409; IG_3.
DR SMART: SM00408; IG_3.
DR PROSITE: PS00835; IG-LIKE; 3.
SQ SEQUENCE 333 AA; 36915 MW; D7C1102P46D08492 CRC64;

```

Query Match 75.1%; Score 1715; DB 4; Length 333;
 Best Local Similarity 100.0%; Pred. No. 2.2e-138;
 Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 MASVVLPSGSCQCAAAAAAAPPGLRLRLLLLSAALLPTGCGQLFTKDVTVIEGVA 60
Db 1 MASVVLPSGSCQCAAAAAAAPPGLRLRLLLLSAALLPTGCGQLFTKDVTVIEGVA 60
Qy 61 TISQVVKSDSDSVIQLNPNRQTIYFDFRPLKDSRQLNLFSSSELKVLNVS:ISDEG 120
Db 61 TISQVVKSDSDSVIQLNPNRQTIYFDFRPLKDSRQLNLFSSSELKVLNVS:ISDEG 120
Qy 121 RYFCQLYTDPPOESYTTITVLVPPRNLMDIQKDTAVEGEIEVNCSTAMASKPATIIRMF 180
Db 121 RYFCQLYTDPPOESYTTITVLVPPRNLMDIQKDTAVEGEIEVNCSTAMASKPATIIRMF 180
Qy 181 KGNTELKGSKEVEBWSMNTVTISQLMKVHKEDGVPVICOVHPAVTGNLQTORYLEVO 240
Db 181 KGNTELKGSKEVEBWSMNTVTISQLMKVHKEDGVPVICOVHPAVTGNLQTORYLEVO 240
Qy 241 YKPOVHIQMTYPIQGLTRBGDALELTCEAIGKQPVMVTVVRVDEMPQHAVLSGNLFI 300
Db 241 YKPOVHIQMTYPIQGLTRBGDALELTCEAIGKQPVMVTVVRVDEMPQHAVLSGNLFI 300
Qy 301 NNINKTDNGTYRCEASNIVGKASHDYLVIYDPTTATTEPVRHGLTQLPNSAELEBDESD 360
Db 301 NNINKTDNGTYRCEASNIVGKASHDYLVIYDPTTATTEPVRHGLTQLPNSAELEBDESD 360

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RESULT 8
Q80VG4 ID Q80VG4 PRELIMINARY; PRT; 336 AA.
AC Q80VG4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE A secretion form of SGISGF/TSIC1.
GN SGISGF/TSIC1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Spleen cell-derived;
RA Ito A., Koma Y., Nagano T.;
RT "A secretion form of SGISGF/TSIC1."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB092414; BAC66173.1; -
DR InterPro: IPR003599; IG_1like.
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003598; IG_c2.
DR Pfam: PF00047; IG_3.
DR SMART: SM00409; IGc2; 3.
DR SMART: SM00408; IGc2; 3.
DR PROSITE: PS50835; IG_LIKE; 3.
SQ SEQUENCE 336 AA; 37155 MW; 9EF3D8B8B5E8F72 CRC64;

Query Match
Best Local Similarity 73.7%; Score 1683.5; DB 11; Length 336;
Matches 327; Conservative 0; Mismatches 4; Indels 3; Gaps 1;

QY 1 MASVTLPSGSGCCAA---AAAAAPGRLRLLLLFSAALIFPTGQGNLFTKDYVIEG 57
DB 1 MASAVLPSGSGCCAAAVAAAPGRLRLLLLSAALIFPTGQGNLFTKDYVIEG 60
QY 58 EVATISQVNSKSDSVIQLNPNROTIFRFRPLKDSRFQNLNFSSELKVLTVNSIS 117
DB 61 EVATISQVNSKSDSVIQLNPNROTIFRFRPLKDSRFQNLNFSSELKVLTVNSIS 120
QY 118 DEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIKQTAVEGEIEVNCAMASKPATTI 177
DB 121 DEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIKQTAVEGEIEVNCAMASKPATTI 180
QY 178 RWFKGNTELGKSKSEVSEMSDMYTVTSQMLKVKHEDDGVVICQVEHPATVGNLTOTQRYL 237
DB 181 RWFKGNTELGKSKSEVSEMSDMYTVTSQMLKVKHEDDGVVICQVEHPATVGNLTOTQRYL 240
QY 238 EVOYKPOVHIQMTYPLQGLTREGDALFELTCEAIGKPPQVMTWVRVDEMPQHAVALSGPN 297
DB 241 EVOYKPOVHIQMTYPLQGLTREGDALFELTCEAIGKPPQVMTWVRVDEMPQHAVALSGPN 300
QY 298 LFNNLNKTDNGTYRCEASNIYGAHSDYMLVYV 331
DB 301 LFNNLNKTDNGTYRCEASNIYGAHSDYMLVYV 334

RESULT 9
Q9D6E7 ID Q9D6E7 PRELIMINARY; PRT; 336 AA.
AC Q9D6E7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 2900073G06RIK protein.
GN IGSF4 OR 2900073G06RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
```

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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa K., Iizawa M., Fukunishi Y., Kono H., Adachi S., Yamanka I.,
RA Saiko T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Caavaent T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuenli P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli R., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
RA Blake J., Boffelli D., Boujunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.T., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Nombarts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wymshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL: AK013775; BAB28988.1; -
DR MGI: 1889272; 198f4.
DR GO: GO:0045202; C:synaptic junction; IDA.
DR GO: GO:0008021; C:synaptic vesicle; IDA.
DR CO: CO:0016347; P:calcium-independent cell adhesion molecule . . . IDA.
DR GO: GO:0005515; P:protein binding; IPI.
DR GO: GO:0007155; P:cell adhesion; IDA.
DR GO: GO:0007416; P:synapticogenesis; IDA.
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003598; IG_c2.
DR Pfam: PF00047; IG_3.
DR SMART: SM00408; IGc2; 1.
DR PROSITE: PS50835; IG_LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 336 AA; 37157 MW; FF887FAFAEFDF120 CRC64;

Query Match
Best Local Similarity 73.2%; Score 1671.5; DB 11; Length 336;
Matches 325; Conservative 0; Mismatches 6; Indels 3; Gaps 1;

QY 1 MASVTLPSGSGCCAA---AAAAAPGRLRLLLLFSAALIFPTGQGNLFTKDYVIEG 57
DB 1 MASAVLADGSCCAAAVAAAPGRLRLLLLSAALIFPTGQGNLFTKDYVIEG 60
QY 58 EVATISQVNSKSDSVIQLNPNROTIFRFRPLKDSRFQNLNFSSELKVLTVNSIS 117
DB 61 EVATISQVNSKSDSVIQLNPNROTIFRFRPLKDSRFQNLNFSSELKVLTVNSIS 120
QY 118 DEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIKQTAVEGEIEVNCAMASKPATTI 177
DB 121 DEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIKQTAVEGEIEVNCAMASKPATTI 180
QY 178 RWFKGNTELGKSKSEVSEMSDMYTVTSQMLKVKHEDDGVVICQVEHPATVGNLTOTQRYL 237
DB 181 RWFKGNTELGKSKSEVSEMSDMYTVTSQMLKVKHEDDGVVICQVEHPATVGNLTOTQRYL 240
QY 238 EVOYKPOVHIQMTYPLQGLTREGDALFELTCEAIGKPPQVMTWVRVDEMPQHAVALSGPN 297
DB 241 EVOYKPOVHIQMTYPLQGLTREGDALFELTCEAIGKPPQVMTWVRVDEMPQHAVALSGPN 300
QY 298 LFNNLNKTDNGTYRCEASNIYGAHSDYMLVYV 331
DB 301 LFNNLNKTDNGTYRCEASNIYGAHSDYMLVYV 334

RESULT 10
Q9Z2H8 ID Q9Z2H8 PRELIMINARY; PRT; 295 AA.
AC Q9Z2H8;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
```

DT 01-MAY-1999 (Tremblrel. 10, last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, last annotation update)
 DE Necln-like protein 2.
 GN IGSF4 OR NECL2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhou Y., Du G., Chen J., Yuan J., Qiang B.;
 RT "Cloning of a novel cDNA encoding a member of immunosuperfamily."; Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF061260; AAC67243.1; -.
 DR MGD; MGI:1889272; Igsf4.
 DR GO; GO:0045202; C:synaptic junction; IDA.
 DR GO; GO:0008021; C:synaptic vesicle; IDA.
 DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . .; IDA.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0007155; P:cell adhesion; IDA.
 DR GO; GO:0007416; P:synaptogenesis; IDA.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003598; Ig C2.
 DR InterPro: IPR003585; Neurexin-like.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00294; 4.1m; 1.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 295 AA; 32509 MW; 9DBD86F6F6F448 CRC64;

Query Match 66.8%; Score 1526; DB 11; Length 295;
 Best Local Similarity 98.6%; Pred. No. 2.9e-122;
 Matches 291; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 148 MIDIOKTAVEGEIEVNCCTAMASKPATITRMFKGNELKGSVEEEMDMYTSQML 207
 DB 1 MIDIOKTAVEGEIEVNCCTAMASKPATITRMFKGNELKGSVEEEMDMYTSQML 60
 QY 208 KVKHEDDGVPIQVHEPAVTGNLQTORYLEVOYKPVHIOPTYPLQGLTRREGDALELTC 267
 DB 61 KVKHEDDGVPIQVHEPAVTGNLQTORYLEVOYKPVHIOPTYPLQGLTRREGDALELTC 120
 QY 268 EAIKGPQVWVTVRWVDDEMPQHAVLSGPNLFNNLNKTDNGTYRCEASNIYKASHSDYM 327
 DB 121 EAIKGPQVWVTVRWVDDEMPQHAVLSGPNLFNNLNKTDNGTYRCEASNIYKASHSDYM 180
 QY 328 LYYDPEPTIIPPTITTTTTTTTTTTTTTTTTTTTTTDSRAGEGSIKAVDAVIGVAVVAVPA 387
 DB 181 LYYDPEPTIIPPTITTTTTTTTTTTTTTTTTTTTTTDSRAGEGSIKAVDAVIGVAVVAVPA 240
 QY 388 MLCCLIIILGRYFARHKGYFTHEAKGADDAADADTAIIINAEQGQNNSEKKEFYI 442
 DB 241 MLCCLIIILGRYFARHKGYFTHEAKGADDAADADTAIIINAEQGQNNSEKKEFYI 295

RESULT 11

09QYU4 PRELIMINARY; PRT; 306 AA.
 AC 09QYU4
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, last annotation update)
 DE Adhesion protein RA175C.
 GN IGSF4 OR RA175C.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Soyama A., Fujita E., Urabe K., Mukasa T., Kourouku Y., Momoi M.,
 RA Momoi T.;

RT "RA175, a novel neuron specific adhesion protein."; Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AB021966; BAA87916.1; -.
 DR MGD; MGI:1889272; Igsf4.
 DR GO; GO:0045202; C:synaptic junction; IDA.
 DR GO; GO:0008021; C:synaptic vesicle; IDA.
 DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . .; IDA.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0007155; P:cell adhesion; IDA.
 DR GO; GO:0007416; P:synaptogenesis; IDA.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003598; Ig_C2.
 DR InterPro: IPR003585; Neurexin-like.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00294; 4.1m; 1.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 306 AA; 33522 MW; A4CB37B0F23554D5 CRC64;

Query Match 65.9%; Score 1503.5; DB 11; Length 306;
 Best Local Similarity 94.8%; Pred. No. 2.5e-120;
 Matches 290; Conservative 2; Mismatches 3; Indels 11; Gaps 1;

QY 148 MIDIOKTAVEGEIEVNCCTAMASKPATITRMFKGNELKGSVEEEMDMYTSQML 207
 DB 1 MIDIOKTAVEGEIEVNCCTAMASKPATITRMFKGNELKGSVEEEMDMYTSQML 60
 QY 208 KVKHEDDGVPIQVHEPAVTGNLQTORYLEVOYKPVHIOPTYPLQGLTRREGDALELTC 267
 DB 61 KVKHEDDGVPIQVHEPAVTGNLQTORYLEVOYKPVHIOPTYPLQGLTRREGDALELTC 120
 QY 268 EAIKGPQVWVTVRWVDDEMPQHAVLSGPNLFNNLNKTDNGTYRCEASNIYKASHSDYM 327
 DB 121 EAIKGPQVWVTVRWVDDEMPQHAVLSGPNLFNNLNKTDNGTYRCEASNIYKASHSDYM 180
 QY 328 LYYDPEPTIIPPTITTTTTTTTTTTTTTTTTTTTTTDSRAGEGSIKAVDAVIGVAVVAVPA 376
 DB 181 LYYDPEPTIIPPTITTTTTTTTTTTTTTTTTTTTTTDSRAGEGSIKAVDAVIGVAVVAVPA 240
 QY 377 IGVVAVVAVVAMLCCLIIILGRYFARHKGYFTHEAKGADDAADADTAIIINAEQGQNNSE 436
 DB 241 IGVVAVVAVVAMLCCLIIILGRYFARHKGYFTHEAKGADDAADADTAIIINAEQGQNNSE 300
 QY 437 KKEEYFI 442
 DB 301 KKEEYFI 306

RESULT 12

09QYU6 PRELIMINARY; PRT; 295 AA.
 AC 09QYU6
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, last annotation update)
 DE Adhesion protein RA175A.
 GN IGSF4 OR RA175A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Soyama A., Fujita E., Urabe K., Mukasa T., Kourouku Y., Momoi M.,
 RA Momoi T.;

DR GO: GO:0005515; F:protein binding; IPI.
 DR GO: GO:0007155; P:cell adhesion; IDA.
 DR GO: GO:0007416; P:synaptogenesis; IDA.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003598; IG_c2.
 DR InterPro: IPR003585; Neurexin-like.
 DR Pfam: PF00047; IG_2.
 DR SMART: SM00294; 4.1m; 1.
 DR SMART: SM00408; IGC2; 1.
 DR PROSITE: PS50835; IG-LIKE; 2.
 DR Immunoglobulin domain.
 SQ SEQUENCE 295 AA; 32347 MW; FDD9E8145C6B971B CRC64;

Query Match 65.0%; Score 1483; DB 11; Length 295;
 Best Local Similarity 95.9%; Pred. No. 1.4e-118;
 Matches 283; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 148 MIDIQDTAVGEIEVNCCTAMASKPATITRMFKGNTELKGSKEVEEWSDMYTTSQML 207
 DB 1 MIDIQDTAVGEIEVNCCTAMASKPATITRMFKGNTELKGSKEVEEWSDMYTTSQML 60
 QY 208 KHKEDDGVPIQVEHPAVTGNLQTORYLEVQKPVQVHIQMTYPLQGLTREGDALELTC 267
 DB 61 KHKEDDGVPIQVEHPAVTGNLQTORYLEVQKPVQVHIQMTYPLQGLTREGDALELTC 120
 QY 268 EAIGKPOVMTWVRVDEMPQHAVLSGPNLFINNKTNDGTGRCEASNVGKASDYM 327
 DB 121 EAIGKPOVMTWVRVDEMPQHAVLSGPNLFINNKTNDGTGRCEASNVGKASDYM 180
 QY 328 LVYVDPPTTIPPTTT 367
 DB 181 LVYVDPPTTIPPTTT 240
 QY 388 MLCILIIIGRYFARKGTFTFHEAKGADDAADDTAIIINAGGONNSEKKKEYFI 442
 DB 241 MLCILIIIGRYFARKGTFTFHEAKGADDAADDTAIIINAGGONNSEKKKEYFI 295

RESULT 13

ID 09QYL5 PRELIMINARY; PRT; 289 AA.

AC 09QYL5
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Adhesion protein RA175B.
 GN IGSP4 OR RA175B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Soyama A., Fujita E., Urase K., Mukasa T., Kourouku Y., Momoi M.,
 RA Momoi T.;
 RT "RA175, a novel neuron specific adhesion protein."
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB021965; BAA87915.1; -.
 DR MGD; MGI:1889272; IGsf4.
 DR GO: GO:0045202; C:synaptic junction; IDA.
 DR GO: GO:0008021; C:synaptic vesicle; IDA.
 DR GO: GO:0016347; F:calcium-independent cell adhesion molecule . . . ; IDA.
 DR GO: GO:0005515; F:protein binding; IPI.
 DR GO: GO:0007155; P:cell adhesion; IDA.
 DR GO: GO:0007416; P:synaptogenesis; IDA.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003598; IG_c2.
 DR InterPro: IPR003585; Neurexin-like.
 DR Pfam: PF00047; IG_2.
 DR SMART: SM00294; 4.1m; 1.
 DR SMART: SM00408; IGC2; 1.
 DR PROSITE: PS50835; IG-LIKE; 2.
 KW Immunoglobulin domain.

SQ SEQUENCE 289 AA; 31811 MW; 8D1B836D0565A84 CRC64;

Query Match 61.1%; Score 1394; DB 11; Length 289;
 Best Local Similarity 91.9%; Pred. No. 5.6e-111;
 Matches 271; Conservative 3; Mismatches 15; Indels 6; Gaps 1;

QY 148 MIDIQDTAVGEIEVNCCTAMASKPATITRMFKGNTELKGSKEVEEWSDMYTTSQML 207
 DB 1 MIDIQDTAVGEIEVNCCTAMASKPATITRMFKGNTELKGSKEVEEWSDMYTTSQML 60
 QY 208 KHKEDDGVPIQVEHPAVTGNLQTORYLEVQKPVQVHIQMTYPLQGLTREGDALELTC 267
 DB 61 KHKEDDGVPIQVEHPAVTGNLQTORYLEVQKPVQVHIQMTYPLQGLTREGDALELTC 120
 QY 268 EAIGKPOVMTWVRVDEMPQHAVLSGPNLFINNKTNDGTGRCEASNVGKASDYM 327
 DB 121 EAIGKPOVMTWVRVDEMPQHAVLSGPNLFINNKTNDGTGRCEASNVGKASDYM 180
 QY 328 LVYVDPPTTIPPTTT 367
 DB 181 LVYVDPPTTIPPTTT 234
 QY 388 MLCILIIIGRYFARKGTFTFHEAKGADDAADDTAIIINAGGONNSEKKKEYFI 442
 DB 235 MLCILIIIGRYFARKGTFTFHEAKGADDAADDTAIIINAGGONNSEKKKEYFI 289

RESULT 14

ID 09QYL3 PRELIMINARY; PRT; 278 AA.

AC 09QYL3
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Adhesion protein RA175N.
 GN IGSP4 OR RA175N.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Soyama A., Fujita E., Urase K., Mukasa T., Kourouku Y., Momoi M.,
 RA Momoi T.;
 RT "RA175, a novel neuron specific adhesion protein."
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB021967; BAA87917.1; -.
 DR MGD; MGI:1889272; IGsf4.
 DR GO: GO:0045202; C:synaptic junction; IDA.
 DR GO: GO:0008021; C:synaptic vesicle; IDA.
 DR GO: GO:0016347; F:calcium-independent cell adhesion molecule . . . ; IDA.
 DR GO: GO:0005515; F:protein binding; IPI.
 DR GO: GO:0007155; P:cell adhesion; IDA.
 DR GO: GO:0007416; P:synaptogenesis; IDA.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003598; IG_c2.
 DR InterPro: IPR003585; Neurexin-like.
 DR Pfam: PF00047; IG_2.
 DR SMART: SM00294; 4.1m; 1.
 DR SMART: SM00408; IGC2; 1.
 DR PROSITE: PS50835; IG-LIKE; 2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 278 AA; 30636 MW; A295F4DEA2724B04 CRC64;

Query Match 60.0%; Score 1370.5; DB 11; Length 278;
 Best Local Similarity 90.2%; Pred. No. 5.4e-105;
 Matches 266; Conservative 3; Mismatches 9; Indels 17; Gaps 1;

QY 148 MIDIQDTAVGEIEVNCCTAMASKPATITRMFKGNTELKGSKEVEEWSDMYTTSQML 207
 DB 1 MIDIQDTAVGEIEVNCCTAMASKPATITRMFKGNTELKGSKEVEEWSDMYTTSQML 60
 QY 208 KHKEDDGVPIQVEHPAVTGNLQTORYLEVQKPVQVHIQMTYPLQGLTREGDALELTC 267

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Db 61 KKHEDGVPIQVEHPATGNLQTRYLEVOYKPOVHIQMTYPLQGLTREGDALELTC 120
Qy 268 EAIKQPQVMTVWVRVDDEPQHAVALSGPMLFINNINKTNGTYRCEASNIYVKAHSDYM 327
Db 121 EAIKQPQVMTVWVRVDDEPQHAVALSGPMLFINNINKTNGTYRCEASNIYVKAHSDYI 180
Qy 328 LYVYDPPTTTPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 387
Db 181 LYVYD-----TTATTEPAVHDSRAGEEGTIGAVDHAYIGVAVVAVFA 223
Qy 388 MLCILIIIGRYFAHKGTYFTHAKGADDAADATATINAGGQNNSEKKEYFI 442
Db 224 MLCILIIIGRYFAHKGTYFTHAKGADDAADATATINAGGQNNSEKKEYFI 278
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RESULT 15

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Q8N3J6 PRELIMINARY; PRT; 435 AA.
ID Q8N3J6
AC Q8N3J6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
DE DKFZP761G128.
CN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RC SEQUENCE FROM N. A.
RA Koehrer K., Beyer A., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL834270; CAD38945.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_1ike.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Hypothetical protein; Immunoglobulin domain.
SQ
SEQUENCE 435 AA; 47554 MW; 59DD41B7F34D46 CRC64;
```

Query Match 39.6%; Score 903; DB 4; Length 435;
Best Local Similarity 44.4%; Pred. No. 1.1e-68;
Matches 193; Conservative 76; Mismatches 138; Indels 28; Gaps 7;

```
Qy 29 LLLLESAALIPFG-DGQNLFTKDYVYIEGEVATISQVYKSDSDVYQILNPNROTIFR 87
Db 8 VLAFFYVCGLLQSGSQGFPLTQNTVYVEGTAIITCRVDQNDNTSLQNSNPAQOTLYFD 67
Qy 88 DFRPLKDSRPQLINFSSSELKVALTNVSIISDEGRYFCQLYTDPQESYTTITVLVPRNL 147
Db 68 DKKALRDNRIELVRAHSEHLSISVDVSLDEGQYCSLFTMPVKTSKAYLITVLGVPEKP 127
Qy 148 MIDIQDTAVEGEIEVNCATVASKRPATIRWEKGTTELKGSVEVEWS--DMYVTSQ 204
Db 128 QISGFSPVWEGDLMQUTCKTSGSKPAADIRFKNDEXIKDYKLEEDANKRTFTVST 187
Qy 205 LMLKVAKEDGVAVICQVEHPATGNLQ-TQRYLEYQKPOVHIQMTYPLQGLTREGDAL 263
Db 188 LDFRVYRSDDGVAVICQVEHPATGNLQ-TQRYLEYQKPOVHIQMTYPLQGLTREGDAL 244
Qy 264 ELTCEAIQKQVMTVWVRVDDEPQHAVALSGPMLFINNINKTNGTYRCEASNIYVKA 321
Db 245 ILTCEASKGKPLPEPVMTKDGGLPDPDRMVVSGRELINILFNKKTNGTYRCEANTNIGQ 304
Qy 322 AHSQVNLVYVDPPTTTPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 367
Db 305 SSAEYVLIHVDVNTILPTTIISLTATVTTVALTTSPTTSATTSIRDPNALAQNG 364
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Qy 368 SRAVDHVIQGVAVVAVVFAMLCIIIIIGRYFAHKGTYFTHAKGADDAADATATINA 427
Db 365 P---DHMLIGIYAVVAVVFTLCSIFLGRYLASHKGYLTNEAKGADADPADATATINA 420
Qy 428 EGGQNNSEKKEYFI 442
Db 421 EGSQVNAEKEKEYFI 435
```

Search completed: July 7, 2004, 06:02:44
Job time: 64.8289 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 7, 2004, 05:56:13 ; Search time 77.6694 Seconds
(without alignments)
1607.918 Million cell updates/sec

Title: US-10-622-237-2

Sequence: 1 MASVLPSSGSCAAAAA.....ATINAGQNNSEKKEVFI 442

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2283	100.0	442	3 AAB25619	Aab25619 Protein e
2	2283	100.0	442	3 AAY94341	Aay94341 Human cel
3	2283	100.0	442	3 AAY45092	Aay45092 Human lym
4	2283	100.0	442	5 AAEL19887	Aael19887 Human tum
5	2283	100.0	442	5 ABP62825	Abp62825 Human pol
6	2283	100.0	442	6 ADA27144	Ada27144 Human nov
7	2283	100.0	442	7 ADE54238	Ade54238 Human pro
8	2283	100.0	442	8 ADE86685	Ade86685 Novel hum
9	2280	99.9	442	6 ABO07196	Ab007196 Human p53
10	2280	99.9	442	7 ADE61605	Ade61605 Human pro
11	2280	99.9	442	7 ADE61608	Ade61608 Human pro
12	2280	99.9	442	2 AAY17830	Aay17830 Human pro
13	2263	99.1	440	2 AAB01321	Aab01321 Human PRO
14	2263	99.1	440	4 AAB25619	Aab25619 Human PRO
15	2263	99.1	440	6 AAB05416	Aab05416 Human PRO
16	2263	99.1	440	6 AAB05416	Aab05416 Human PRO
17	2263	99.1	440	6 AAB05416	Aab05416 Human PRO
18	2263	99.1	440	6 AAB05416	Aab05416 Human PRO
19	2263	99.1	440	6 AAB05416	Aab05416 Human PRO
20	2263	99.1	440	6 AAB05416	Aab05416 Human PRO
21	2263	99.1	440	6 AAB05416	Aab05416 Human PRO
22	2263	99.1	440	6 AAB05416	Aab05416 Human PRO
23	2263	99.1	440	6 AAB05416	Aab05416 Human PRO
24	2263	99.1	440	6 AAB05416	Aab05416 Human PRO
25	2263	99.1	440	6 AAB05416	Aab05416 Human PRO

ALIGNMENTS

26	2263	99.1	440	6 AAB05416	Abu96145 Novel hum
27	2263	99.1	440	6 AAB05416	Abu92576 Human sec
28	2263	99.1	440	6 AAB05416	Abu08653 Human sec
29	2263	99.1	440	6 AAB05416	Abu02705 Human sec
30	2263	99.1	440	6 AAB05416	Abu74859 Human sec
31	2263	99.1	440	6 AAB05416	Abu94621 Human sec
32	2263	99.1	440	6 AAB05416	Abu60240 Human PRO
33	2263	99.1	440	6 AAB05416	Abu85594 Human PRO
34	2263	99.1	440	6 AAB05416	Abu98754 Novel hum
35	2263	99.1	440	6 AAB05416	Abu97969 Novel hum
36	2263	99.1	440	6 AAB05416	Abu91675 Novel hum
37	2263	99.1	440	6 AAB05416	Abu89368 Human PRO
38	2263	99.1	440	6 AAB05416	Abu86309 Human PRO
39	2263	99.1	440	6 AAB05416	Abu67422 Human sec
40	2263	99.1	440	6 AAB05416	Abu80450 Human PRO
41	2263	99.1	440	6 AAB05416	Abu99368 Human PRO
42	2263	99.1	440	6 AAB05416	Abu98758 Human sec
43	2263	99.1	440	6 AAB05416	Abu16281 Human sec
44	2263	99.1	440	6 AAB05416	Abu92181 Human sec
45	2263	99.1	440	6 AAB05416	Abu18822 Human sec

RESULT 1

ID AAB25619 standard, protein, 442 AA.

21-NOV-2000 (first entry)

Protein encoded by human secreted protein gene #11.

Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic;
antirheumatic; dermatological; antiproliferative; antiarteriosclerotic;
anticancer; vulnery; antiviral; antibacterial; antifungal;
immune disorder; Addison's disease; rheumatoid arthritis; dermatitis;
multiple sclerosis; inflammatory disorder; inflammatory bowel disease;
Crohn's disease; nephritis; hyperproliferative disorder;
cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer;
melanoma; lymphoma; wound healing; human.

Homo sapiens.

WO200029435-A1.

25-MAY-2000.

27-OCT-1999; 99WO-US025031.

28-OCT-1998; 98US-0105971P.

(HUMA-) HUMAN GENOME SCI INC.

Ni J, Ruben SM, Olsen HS, Young PE, Kenny JJ, Moore PA, Wei Y,
Greene JM;

WPI; 2000-387742/33.

Isolated nucleic acid molecules encoding human secreted proteins are used
for the prevention, amelioration and treatment of autoimmune,
inflammatory, hyperproliferative and cardiovascular disorders, cancer,
wounds, and infectious diseases.

Disclosure; Page 182-183; 803pp; English.

The present invention relates to 12 secreted human proteins and the
nucleotide sequences encoding them. The polynucleotide sequences given in
CC AAB0606-A80623 encode the 12 secreted protein sequences given in
CC AAB2576-B25593. The human secreted proteins have various activities
dependent on the tissues in which they are expressed. Examples of the

CC activities of the proteins include: immunosuppressant; anti-inflammatory;
 CC antiarthritic; antirheumatic; dermatological; antiproliferative;
 CC antitumor; antileukemic; anticancer; antineoplastic; antiviral; antibacterial;
 CC antifungal activity. The proteins, polypeptides, agonists and
 CC antagonists may be used to treat prevent and/or diagnose various diseases,
 CC disorders and conditions examples of which include: immune disorders e.g.
 CC Addison's disease, rheumatoid arthritis, dermatitis, and multiple
 CC sclerosis; inflammatory disorders e.g. inflammatory bowel disease,
 CC Crohn's disease and nephritis; hyperproliferative disorders such as
 CC paraneoplasia and myeloid leukemia; cardiovascular disorders e.g. coronary
 CC artery disease and myocarditis; cancer e.g. melanoma and lymphoma. The
 CC proteins and polynucleotide sequences may also be used in wound healing
 CC and the treatment of infectious diseases. The human secreted protein gene
 CC #11 and protein sequences are represented in sequences AAA80616 and
 CC AAA80617. Sequences AAA80677-AAA80682 represent genes related to the
 CC secreted protein gene#11
 CC
 XX Sequence 442 AA:

Query Match 100.0%; Score 2283; DB 3; Length 442;
 Best Local Similarity 100.0%; Pred. No. 5, 8e-158;
 Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASVLPSSGSCAAAAAARPGRLRLDLLLPSAALFTGSDQNLFTKDYVLEGEVA 60
 DB 1 MASVLPSSGSCAAAAAARPGRLRLDLLLPSAALFTGSDQNLFTKDYVLEGEVA 60
 QY 61 TISQVVKSDSVYQLNPNRQTIYPRDFRPLKDSRQNLNFSSELKXSLTNVSLSDG 120
 DB 61 TISQVVKSDSVYQLNPNRQTIYPRDFRPLKDSRQNLNFSSELKXSLTNVSLSDG 120
 QY 121 RYFQQLYDPPQESYTTITLVLPFRNLMDIQKDTVEGEIIVNCTAMASKPATIRMF 180
 DB 121 RYFQQLYDPPQESYTTITLVLPFRNLMDIQKDTVEGEIIVNCTAMASKPATIRMF 180
 QY 121 RYFQQLYDPPQESYTTITLVLPFRNLMDIQKDTVEGEIIVNCTAMASKPATIRMF 180
 DB 121 RYFQQLYDPPQESYTTITLVLPFRNLMDIQKDTVEGEIIVNCTAMASKPATIRMF 180
 QY 181 KGNTELKGSBEVBSMTVTTSQMLKFAKEDDGVICQVHPAVTGNLTQRYLAVQ 240
 DB 181 KGNTELKGSBEVBSMTVTTSQMLKFAKEDDGVICQVHPAVTGNLTQRYLAVQ 240
 QY 181 KGNTELKGSBEVBSMTVTTSQMLKFAKEDDGVICQVHPAVTGNLTQRYLAVQ 240
 DB 181 KGNTELKGSBEVBSMTVTTSQMLKFAKEDDGVICQVHPAVTGNLTQRYLAVQ 240
 QY 241 YKPOVHQMTPYPLQGLTRFDALFLCEAIGKQPMVWTVRVDDEMPQAVLSGNLTI 300
 DB 241 YKPOVHQMTPYPLQGLTRFDALFLCEAIGKQPMVWTVRVDDEMPQAVLSGNLTI 300
 QY 241 YKPOVHQMTPYPLQGLTRFDALFLCEAIGKQPMVWTVRVDDEMPQAVLSGNLTI 300
 DB 241 YKPOVHQMTPYPLQGLTRFDALFLCEAIGKQPMVWTVRVDDEMPQAVLSGNLTI 300
 QY 301 NNLLKTDNGTGRCAASNIYVKAHSDYMLVYDPTTIPPTTTTTTTTTTTTTITD 360
 DB 301 NNLLKTDNGTGRCAASNIYVKAHSDYMLVYDPTTIPPTTTTTTTTTTTTTITD 360
 QY 361 SRAGEBSIRAVDPAVIGVAVVAVPAMCLLILGRYFARHKGTFTHBAKGADDA 420
 DB 361 SRAGEBSIRAVDPAVIGVAVVAVPAMCLLILGRYFARHKGTFTHBAKGADDA 420
 QY 421 DTALINAEQQNNSEKKEYFI 442
 DB 421 DTALINAEQQNNSEKKEYFI 442

RESULT 2
 ID AAY94341 standard; protein; 442 AA.

AC AAY94341:

XX 22-AUG-2000 (first entry)
 DE Human cell surface receptor protein #8.
 XX Human; HCSR; cytosolic; antirheumatic; antineoplastic; antileukemic;
 XX immunosuppressant; antitumor; antineoplastic; antibacterial; antiparasitic;
 XX neuroprotective; nocitopic; anticomulant; cancer; leukemia; melanoma;
 XX rheumatoid arthritis; asthma; atherosclerosis; akathesia;
 XX Alzheimer's diseases; multiple sclerosis; epilepsy.
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..44
 FT Peptide 45..442
 FT Protein /label=HCSR-8
 FT Region 53
 FT /note="potential phosphorylation site"
 FT /label=Immunoglobulin_domain
 FT /note="potential glycosylation site"
 FT Region 67
 FT /note="potential glycosylation site"
 FT Region 101
 FT /note="potential glycosylation site"
 FT Region 103
 FT /note="potential glycosylation site"
 FT Region 113
 FT /note="potential glycosylation site"
 FT Region 115
 FT /note="potential glycosylation site"
 FT Region 155
 FT /note="potential phosphorylation site"
 FT Region 159..222
 FT /label=Immunoglobulin_domain
 FT /note="potential glycosylation site"
 FT Region 176
 FT /note="potential phosphorylation site"
 FT Region 190
 FT /note="potential phosphorylation site"
 FT Region 233
 FT /note="potential phosphorylation site"
 FT Region 241
 FT /note="potential phosphorylation site"
 FT Domain 260..315
 FT /label=Immunoglobulin_domain
 FT /note="potential glycosylation site"
 FT Region 304
 FT /note="potential glycosylation site"
 FT Region 308
 FT /note="potential glycosylation site"
 FT Region 310
 FT /note="potential phosphorylation site"
 FT Region 329
 FT /note="potential phosphorylation site"
 FT Region 368
 FT /note="potential phosphorylation site"
 FT Domain 375..394
 FT /label=Transmembrane_domain
 FT Region 432
 FT /note="potential glycosylation site"
 XX WO20028032-A2.
 XX 18-MAY-2000.
 XX PD 12-NOV-1999; 99WO-US026742.
 XX PF 12-NOV-1999; 98US-00191280.
 XX PR 07-DEC-1998; 98US-00206647.
 XX PR 08-MAR-1999; 99US-0123404P.
 XX PA (INCY-) INCYTE PHARM INC.
 XX Tang YT, Corley NC, Guegler KU, Yue H, Baughn MR, Lal P;
 XX Hillman JL, Bandman O, Azimzai Y, Au-Young J;
 XX WPI; 2000-376546/32.
 XX N-PSDB; AAA27051.
 XX New human cell surface receptor protein and polynucleotide useful for
 XX diagnosis, prevention and treatment of cancer, immune disorders,
 XX infection and neuronal disorders.

PS Claim 1; Page 81-82; 97pp; English.

The present sequence is a novel human cell surface receptor protein (HCSR) designated HCSR-8. The nucleotide sequence was identified in Incyte clone j12256 from the cDNA library LUNG0702, which was made from RNA isolated from lung tissue. A number of Incyte Clones were used to assemble the consensus sequence. BLAST analysis showed that the sequence is homologous to immuno-superfamily protein B12 g3179242. HCSR and its antagonist are useful for preventing or treating disorders associated with decreased or increased expression or activity of HCSR. Such disorders include cancers such as leukaemia and melanoma, immune disorders such as rheumatoid arthritis, asthma and atherosclerosis, bacterial and parasitic infections and neuronal disorders such as Alzheimer's disease, multiple sclerosis and epilepsy. Polynucleotides encoding HCRPs may be used as hybridisation probes to diagnose these conditions. Anti-HCSR antibodies may be used as antagonists, as a targeting or delivery mechanism for bringing pharmaceutical agents into contact with cells or tissues expressing HCSR and for diagnosis of HCSR-related disorders. HCSR and its catalytic or immunogenic fragments are useful for drug screening using libraries of compounds

5Q Sequence 442 AA;

Query Match	100.0%	Score 2283	DB 3	Length 442
Best Local Similarity	100.0%	Pred. No. 5.8e-158		
Matches 442	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	1	MSVLPSSSQCAAAAAPGLRLRLLLFSAAPALIPGDGNNLTQVTVIEGVA	60
Db	1	MSVLPSSSQCAAAAAPGLRLRLLLFSAAPALIPGDGNNLTQVTVIEGVA	60
QY	61	TISQVNSKDDSVIQLNNRNQTIYFRDFRPLKDSFQLNFFSSSELKVSJTNVISDEG	120
Db	61	TISQVNSKDDSVIQLNNRNQTIYFRDFRPLKDSFQLNFFSSSELKVSJTNVISDEG	120
QY	121	RYSCQIYTPRPSSTYTTITVLVPRPNLMDIQKQNAVGEELVNVCTMAKSPATTRMF	180
Db	121	RYSCQIYTPRPSSTYTTITVLVPRPNLMDIQKQNAVGEELVNVCTMAKSPATTRMF	180
QY	181	KGNTELKGRSEVENSDMTVTSQMLTKVHKEDDQVPIQVEHPAVTGNQTORYLEVQ	240
Db	181	KGNTELKGRSEVENSDMTVTSQMLTKVHKEDDQVPIQVEHPAVTGNQTORYLEVQ	240
QY	241	YKQVNIQMTYPRQGITREGDMLTELCEALIGKRPQVMTVYRVDEMFQHAISGNLFI	300
Db	241	YKQVNIQMTYPRQGITREGDMLTELCEALIGKRPQVMTVYRVDEMFQHAISGNLFI	300
QY	301	NNLNKTDNGYRCEASNIVGKASHDMLVYVDPRTTTPRTTTTTTTTTTLTLITD	360
Db	301	NNLNKTDNGYRCEASNIVGKASHDMLVYVDPRTTTPRTTTTTTTTTTLTLITD	360
QY	361	SRAGEGSIKAVDHAIVGVAVVVFAMCLLIIIGRYFARHKGYTFTHAKGADADA	420
Db	361	SRAGEGSIKAVDHAIVGVAVVVFAMCLLIIIGRYFARHKGYTFTHAKGADADA	420
QY	421	DTALINABGGUNNSEKKEFYI 442	
Db	421	DTALINABGGUNNSEKKEFYI 442	

RESULT 3

ID AAY45092 standard; protein; 442 AA.

AA AC AA45092

DT 31-MAY-2000 (first entry)

Human lymphoid derived dendritic cell adhesion molecule

XX Lymphoid derived dendritic cell adhesion molecule: LDCAM: human: B7-1:

B7-1; T cell proliferation; natural killer cell; NK; tumour cell;

KM biological activity; quality control reagent; treatment; inflammation;
 KW immune system disorder; autoimmune; viral infection; infectious disease;
 KW organ transplant rejection; bone marrow; modulator; immune response.
 XX
 XS Homo sapiens.

OS Homo sapiens

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100	100

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The present amino acid sequence is the human lymphoid derived dendritic cell adhesion molecule, LDCAM. It is found on lymphoid derived dendritic cells and displays homology to adhesion molecules, B7-1 and cytoplasmic region of B7-1. Human LDCAM is expressed in breast, retina, foetal liver, spleen and heart, lung, muscle, placenta, thyroid and lung carcinoma. LDCAM polypeptides interacts with T cell surface molecules to alter signalling and inhibits T cell proliferation, bind to themselves and B7-1, an LDCAM binding protein and increases natural killer (NK) cell populations. It may be used to measure the biological activity and as quality control reagents of LDCAM binding proteins. LDCAM may be used for treating disorders associated with malfunctioning of immune system, inflammation, autoimmune disorders, viral infected cells, infectious diseases and for killing tumour cells. They are also useful for prevention or reducing the effect of organ and bone marrow transplant rejection and for modulating T cell immune responses. LDCAM polypeptides may also be used as carriers for delivering agents attached to T cells or cells bearing B7-1.

Sequence 442 AA:

```
Query Match      100.0%; Score 2283; DB 3; Length 442;
Best Local Similarity 100.0%; Pred. No. 5.8e-15;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0
```

QY 1 MASVLPESGSCAAAAAAPPGLRLRLLLLSAALIFPGDQNLFTKDVVIEGEVA 60
 DB 1 MASVLPESGSCAAAAAAPPGLRLRLLLLSAALIFPGDQNLFTKDVVIEGEVA 60
 QY 61 TISGVNKSDDSVIQLNPNRQTIYFRDPRPLKDSRFQLNFSSELKSLTNVSIISDEG 120
 DB 61 TISGVNKSDDSVIQLNPNRQTIYFRDPRPLKDSRFQLNFSSELKSLTNVSIISDEG 120
 QY 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIOKDTAVEGEIEVNCNAMASKPATITRMF 180
 DB 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIOKDTAVEGEIEVNCNAMASKPATITRMF 180
 QY 181 KGNTELKGSKEVEEWSMDYVTSQMLKVKHEDDGVVICOVHPAVTGNLQORYLEVO 240
 DB 181 KGNTELKGSKEVEEWSMDYVTSQMLKVKHEDDGVVICOVHPAVTGNLQORYLEVO 240
 QY 241 YKPOVHIQMTYPILOGLIREGDALELTCEAIGKPPQVWVTVWRVDDMPQAVISGPNLFI 300
 DB 241 YKPOVHIQMTYPILOGLIREGDALELTCEAIGKPPQVWVTVWRVDDMPQAVISGPNLFI 300
 QY 301 NNINKTNGTYRCEASNVGKAHSDYMLVYVDPPTIIPPTTTTTTTTTTTTTTTTT 360
 DB 301 NNINKTNGTYRCEASNVGKAHSDYMLVYVDPPTIIPPTTTTTTTTTTTTTTTTT 360
 QY 361 SRAGEGSIKRAVDHAVIGVAVVFPMLCLIIIGRYFARHKGTFTHEAKGADDAADA 420
 DB 361 SRAGEGSIKRAVDHAVIGVAVVFPMLCLIIIGRYFARHKGTFTHEAKGADDAADA 420
 QY 421 DTALINAEAGGQNNSEKKEYFI 442
 DB 421 DTALINAEAGGQNNSEKKEYFI 442

RESULT 4

AAE19887

ID AAE19887 standard; protein; 442 AA.

AAE19887;

DT 18-JUN-2002 (first entry)

DB Human tumour suppressor lung cancer 1 (TSLC1) polypeptide.

QY Human; hepatocellular carcinoma; tumour suppressor lung cancer 1; TSLC1;

DB liver; lung; pancreatic cancer; cell proliferative disorder; cytostatic;

QY gene therapy.

DB Homo sapiens.

QY MO200214557-A1.

DB 21-FEB-2002.

QY 15-AUG-2001; 2001MO-US025690.

DB 15-AUG-2000; 2000US-0225264P.

QY (UJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

DB Reeves RH, Yoshinori M;

QY WPI; 2002-241913/29.

DB Detecting cell proliferative disorder associated with tumor suppressor

QY lung cancer (TSLC) 1 in subject, comprises contacting proliferating cell

DB of subject with reagent detecting TSLC1 and detecting modification in

QY TSLC1 level.

DB Disclosure; Page 49-50; 59pp; English.

QY The invention relates to a method for detecting cell proliferative

DB disorder associated with tumour suppressor lung cancer 1 (TSLC1) in a

CC subject. The method comprising contacting a cell component of a
 CC proliferating cell with a reagent that detects level of the cell
 CC component in the proliferating cell and determining modification in the
 CC level of the cell component in proliferating cell as compared with a
 CC healthy cell, where modification indicates disorder associated with
 CC TSLC1. The method is useful for detecting a cell proliferative disorder
 CC (e.g. liver, lung or pancreatic cancer) associated with tumour suppressor
 CC lung cancer 1 (TSLC1) in a subject. The invention is useful in gene
 CC therapy and for treating a cell proliferative disorder such as lung
 CC cancer (human non-small cell lung cancer), liver cancer (hepatocellular
 CC carcinoma) or pancreatic cancer associated with modification of TSLC1
 CC production, where a reagent which modulates (preferably, increases) TSLC1
 CC level in the cells, is employed. The present sequence is human TSLC1
 CC
 XX Sequence 442 AA:

Query Match 100.0%; Score 2283; DB 5; Length 442;
 Best Local Similarity 100.0%; Pred. No. 5; 8e-158;
 Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASVLPESGSCAAAAAAPPGLRLRLLLLSAALIFPGDQNLFTKDVVIEGEVA 60
 DB 1 MASVLPESGSCAAAAAAPPGLRLRLLLLSAALIFPGDQNLFTKDVVIEGEVA 60
 QY 61 TISGVNKSDDSVIQLNPNRQTIYFRDPRPLKDSRFQLNFSSELKSLTNVSIISDEG 120
 DB 61 TISGVNKSDDSVIQLNPNRQTIYFRDPRPLKDSRFQLNFSSELKSLTNVSIISDEG 120
 QY 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIOKDTAVEGEIEVNCNAMASKPATITRMF 180
 DB 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIOKDTAVEGEIEVNCNAMASKPATITRMF 180
 QY 181 KGNTELKGSKEVEEWSMDYVTSQMLKVKHEDDGVVICOVHPAVTGNLQORYLEVO 240
 DB 181 KGNTELKGSKEVEEWSMDYVTSQMLKVKHEDDGVVICOVHPAVTGNLQORYLEVO 240
 QY 241 YKPOVHIQMTYPILOGLIREGDALELTCEAIGKPPQVWVTVWRVDDMPQAVISGPNLFI 300
 DB 241 YKPOVHIQMTYPILOGLIREGDALELTCEAIGKPPQVWVTVWRVDDMPQAVISGPNLFI 300
 QY 301 NNINKTNGTYRCEASNVGKAHSDYMLVYVDPPTIIPPTTTTTTTTTTTTTTTTT 360
 DB 301 NNINKTNGTYRCEASNVGKAHSDYMLVYVDPPTIIPPTTTTTTTTTTTTTTTTT 360
 QY 361 SRAGEGSIKRAVDHAVIGVAVVFPMLCLIIIGRYFARHKGTFTHEAKGADDAADA 420
 DB 361 SRAGEGSIKRAVDHAVIGVAVVFPMLCLIIIGRYFARHKGTFTHEAKGADDAADA 420
 QY 421 DTALINAEAGGQNNSEKKEYFI 442
 DB 421 DTALINAEAGGQNNSEKKEYFI 442

RESULT 5

ABP62825

ID ABP62825 standard; protein; 442 AA.

AC ABP62825;

DT 14-OCT-2002 (first entry)

DB Human polypeptide SEQ ID NO 262.

QY Human; vulnery; dermatological; neuroprotective; nootropic; cancer;

DB antiparkinsonian; immunostimulant; cytostatic; immunosuppressive;

QY antidiabetic; antiallergic; gene therapy; wound healing; tissue repair;

DB burn; central nervous system disorder; Alzheimer's disease;

QY Parkinson's disease; Huntington's disease; immune disorder;

DB autoimmune disorder; multiple sclerosis; diabetes; allergy.

QY Homo sapiens.

DB WO200218424-A2.

XX 07-MAR-2002.
 PD 31-AUG-2001; 2001WO-US027093.
 XX 01-SEP-2000; 2000US-00654935.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;
 PI Zhao QH, Wang D, Liu C, Drmanac RT, Wehrman T;
 XX WPI; 2002-583321/62.
 DR N-PSDB; ABQ93304.
 XX
 PT New polynucleotide and polypeptides, useful for treatment and diagnosis
 PT of Alzheimer's, Parkinson's, Huntington's, amyotrophic lateral
 PT sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple
 PT sclerosis, diabetes and allergies.
 XX
 PS Claim 20; SEQ ID NO 262; 284bp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated polynucleotide (I) comprising one of
 CC 245 sequences (ABQ93288-ABQ93532). Treating a condition comprising
 CC administering to a mammalian subject a composition comprising the protein
 CC (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II).
 CC (I), (II) and (III) are useful for diagnostic evaluation of disorders.
 CC (I) is useful for gene therapy of diseases and (II) can be used for
 CC therapeutic treatment. Diseases that may be treated include wound healing
 CC and tissue repair, burns, central nervous system disorders (e.g.
 CC Alzheimer's, Parkinson's, Huntington's and amyotrophic lateral
 CC sclerosis), immune deficiencies, cancer, autoimmune disorders, multiple
 CC sclerosis, diabetes and allergies. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SO Sequence 442 AA:
 Query Match 100.0%; Score 2283; DB 5; Length 442;
 Best Local Similarity 100.0%; Pred. No. 5.8e-158;
 Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 421 DTAIINAEQGNNSEKKEYFI 442
 RESULT 6
 ADA27144
 ID ADA27144 standard; protein; 442 AA.
 XX
 AC ADA27144;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human novel secreted protein from gene 11 #3.
 XX
 KW cytostatic; antiinflammatory; immunomodulator; neuroprotective;
 KW hemostatic; gene therapy; cancer; inflammation; immune disorder;
 KW neurological disorder; blood clotting disorder; food additive;
 KW preservative; human; secreted protein.
 XX
 OS Homo sapiens.
 XX
 PN US2003055231-A1.
 XX
 PD 20-MAR-2003.
 XX
 PF 29-OCT-2001; 2001US-00984130.
 XX
 PR 28-OCT-1998; 98US-0105971P.
 PR 27-OCT-1999; 99WO-US025031.
 PR 19-APR-2000; 2000US-0198407P.
 PR 30-OCT-2000; 2000US-0243792P.
 PR 18-APR-2001; 2001US-00836353.
 XX
 PA (NIJ/) NI J.
 PA (YOUNG/) YOUNG P E.
 PA (KENN/) KENNY J J.
 PA (OLSE/) OLSEN H S.
 PA (MOOR/) MOORE P A.
 PA (WEIT/) WEI Y.
 PA (GREE/) GREENE J M.
 PA (RUBE/) RUBEN S M.
 PA (LIU/) LIU D.
 PA (CROC/) CROCKER P R.
 XX
 PI Ni J, Young PE, Kenny JJ, Olsen HS, Moore PA, Wei Y, Greene JM;
 PI Ruben SM, Liu D, Crocker PR;
 XX
 DR WPI; 2003-567103/53.
 XX
 PT New human secreted nucleic acid molecules and polypeptides, useful for
 PT preventing, treating, or ameliorating a medical condition, such as
 PT cancer, inflammation, immune disorders, neurological and blood clotting
 PT disorders.
 XX
 PS Disclosure; Page 72; 454bp; English.
 XX
 CC The invention relates to an isolated nucleic molecule that is at least
 CC 95% identical to 18 human cDNA sequences representing 12 novel genes
 CC encoding secreted proteins or a polynucleotide fragment of the cDNA.
 CC sequence contained in American Type Culture Collection (ATCC) deposit No.
 CC variant of the polynucleotide having a polynucleotide capable of
 CC hybridizing under conditions the polynucleotide, where the polynucleotide
 CC does not hybridize under stringent conditions to a nucleic acid molecule
 CC having a nucleotide sequence of only A or T residues. Also included are
 CC recombinant vectors, host cells (for producing the polypeptide) the
 CC secreted polypeptide (comprising a sequence that is at least 95%
 CC identical to a polypeptide fragment, domain, epitope, full-length
 CC protein, variant, allelic variant or species homologue), antibodies that
 CC specifically bind to the polypeptides, diagnosing, treating, preventing
 CC or ameliorating a medical condition by administering the polynucleotide
 CC or the polypeptide, the gene corresponding to the cDNA sequence and
 CC identifying an activity in a biological assay (by expressing the cDNA
 CC sequence in a cell, isolating the supernatant, and detecting an activity

CC in a biological assay and identifying the protein in the supernatant
 CC having the activity. The polypeptides, nucleic acids and antibodies are
 CC useful for diagnosing a pathological condition or a susceptibility to a
 CC pathological condition, for preventing, treating, or ameliorating a
 CC medical condition, such as cancer, inflammation or other immune
 CC disorders, neuroblast and blood clotting disorders (many examples are
 CC given in the specification). The nucleic acids are also useful for
 CC chromosome identification, radiation hybrid mapping or long-range
 CC restriction mapping. The polypeptides and antibodies are useful for
 CC providing immunological probes for differential identification of the
 CC tissues immunohistochemistry assays. The polypeptide, polynucleotide,
 CC agonist or antagonist may also be used as a food additive or preservative
 CC to increase or decrease storage capabilities, fat content or other
 CC nutritional components. The present is a secreted protein of the
 CC invention.

CC Sequence 442 AA;

Query Match 100.0%; Score 2283; DB 6; Length 442;
 Best Local Similarity 100.0%; Pred. No. 5.8e-158;
 Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 MASVTLPSGSGCAAAAAAPGRLRLRLILFSAALIPFGDQNLFTKDVIVIGEVA 60
 DB 1 MASVTLPSGSGCAAAAAAPGRLRLRLILFSAALIPFGDQNLFTKDVIVIGEVA 60
 QY 61 TISCVNKSDDSVIQLNPNRQTIYFRDPRFKDSRFQNLNFSSELKVSITNVSISDEG 120
 DB 61 TISCVNKSDDSVIQLNPNRQTIYFRDPRFKDSRFQNLNFSSELKVSITNVSISDEG 120
 QY 121 RYFCOLYDPPQESYTTITVLPVRNLMIDIQKDTAVEGEIEVNCNMAKSPATTIRMF 180
 DB 121 RYFCOLYDPPQESYTTITVLPVRNLMIDIQKDTAVEGEIEVNCNMAKSPATTIRMF 180
 QY 121 RYFCOLYDPPQESYTTITVLPVRNLMIDIQKDTAVEGEIEVNCNMAKSPATTIRMF 180
 DB 121 RYFCOLYDPPQESYTTITVLPVRNLMIDIQKDTAVEGEIEVNCNMAKSPATTIRMF 180
 QY 181 KGNTELKSKSEVEEMSDMTVTYSQMLKVHKEDGVVICOVHPAVTGNLQOTRYLEVQ 240
 DB 181 KGNTELKSKSEVEEMSDMTVTYSQMLKVHKEDGVVICOVHPAVTGNLQOTRYLEVQ 240
 QY 241 YKPOVHIQMTYPLQGLTREGDALTECEAIKGPQVWVWTVRVDDEMPQHAVISGNLFI 300
 DB 241 YKPOVHIQMTYPLQGLTREGDALTECEAIKGPQVWVWTVRVDDEMPQHAVISGNLFI 300
 QY 301 NNKKTNDGTYRCASNIIVGKASDMLVYVDPPTTTPPTTTTTTTTTTTTTTTTT 360
 DB 301 NNKKTNDGTYRCASNIIVGKASDMLVYVDPPTTTPPTTTTTTTTTTTTTTTTT 360
 QY 301 NNKKTNDGTYRCASNIIVGKASDMLVYVDPPTTTPPTTTTTTTTTTTTTTTTT 360
 DB 301 NNKKTNDGTYRCASNIIVGKASDMLVYVDPPTTTPPTTTTTTTTTTTTTTTTT 360
 QY 361 SRAGEGSIKRAVDHVAIVGVVAVVFMALCLILIGRYFARHKGTYPTEHAKGADDA 420
 DB 361 SRAGEGSIKRAVDHVAIVGVVAVVFMALCLILIGRYFARHKGTYPTEHAKGADDA 420
 QY 421 DTATINAEQGQNNSEKKEFYI 442
 DB 421 DTATINAEQGQNNSEKKEFYI 442

RESULT 7
 ADE54238
 ID ADE54238 standard; protein; 442 AA.

AC ADE54238;

DT 29-JAN-2004 (first entry)

DE Human Protein NP_055146, SEQ ID NO 41.

XX Human; pain; neuronal tissue; gene therapy;

KM spinal segmental nerve injury; chronic constriction injury; CCI;

XX spared nerve injury; SNI; Chung.

OS Homo sapiens.

XX WO2003016475-A2.

PD 27-FEB-2003.
 PF 14-AUG-2002; 2002WO-US025765.
 XX 14-AUG-2001; 2001US-0312147P.
 XX 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX (GENO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 PI Woolf C, D'urso D, Befort K, Costigan M,
 XX WPI/ 2003-268312/26.
 DR GENBANK, NP_055148.
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 PS Claim 1; Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which differentially
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

CC Sequence 442 AA;

Query Match 100.0%; Score 2283; DB 7; Length 442;
 Best Local Similarity 100.0%; Pred. No. 5.8e-158;
 Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASVTLPSGSGCAAAAAAPGRLRLRLILFSAALIPFGDQNLFTKDVIVIGEVA 60
 DB 1 MASVTLPSGSGCAAAAAAPGRLRLRLILFSAALIPFGDQNLFTKDVIVIGEVA 60
 QY 61 TISCVNKSDDSVIQLNPNRQTIYFRDPRFKDSRFQNLNFSSELKVSITNVSISDEG 120
 DB 61 TISCVNKSDDSVIQLNPNRQTIYFRDPRFKDSRFQNLNFSSELKVSITNVSISDEG 120
 QY 121 RYFCOLYDPPQESYTTITVLPVRNLMIDIQKDTAVEGEIEVNCNMAKSPATTIRMF 180
 DB 121 RYFCOLYDPPQESYTTITVLPVRNLMIDIQKDTAVEGEIEVNCNMAKSPATTIRMF 180
 QY 121 RYFCOLYDPPQESYTTITVLPVRNLMIDIQKDTAVEGEIEVNCNMAKSPATTIRMF 180
 DB 121 RYFCOLYDPPQESYTTITVLPVRNLMIDIQKDTAVEGEIEVNCNMAKSPATTIRMF 180
 QY 181 KGNTELKSKSEVEEMSDMTVTYSQMLKVHKEDGVVICOVHPAVTGNLQOTRYLEVQ 240
 DB 181 KGNTELKSKSEVEEMSDMTVTYSQMLKVHKEDGVVICOVHPAVTGNLQOTRYLEVQ 240
 QY 241 YKPOVHIQMTYPLQGLTREGDALTECEAIKGPQVWVWTVRVDDEMPQHAVISGNLFI 300
 DB 241 YKPOVHIQMTYPLQGLTREGDALTECEAIKGPQVWVWTVRVDDEMPQHAVISGNLFI 300

DB 241 YKPOVHIQMTYPLQGLTREGDALBELTCEAIKGPQPMVMTWVVDDEMPQHAVLSGPNLFI 300
 QY 301 NNLNKTNDGTYRCEASNIWGKAHSDYMLVYVDPPTTTPPTTTTPTTTTTLITLITD 360
 DB 301 NNLNKTNDGTYRCEASNIWGKAHSDYMLVYVDPPTTTPPTTTTPTTTTTLITLITD 360
 QY 361 SRAGEGSIKRAVDHAVIGVAVVVFAMLCILIIIGRYFARHKGTYFTHKAGDADADA 420
 DB 361 SRAGEGSIKRAVDHAVIGVAVVVFAMLCILIIIGRYFARHKGTYFTHKAGDADADA 420
 QY 421 DTALINAEQGQNNSEKKEKYEPI 442
 DB 421 DTALINAEQGQNNSEKKEKYEPI 442

RESULT 8
 ADE86685
 ID ADE86685 standard; protein; 442 AA.
 AC ADE86685;
 XX
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Novel human secreted protein #11 associated protein #1.
 XX
 KM human; secreted protein; cancer; liver disorder; hepatitis;
 KM neutral disorder; Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 PN US2003129685-A1.
 PD 10-JUL-2003.
 XX
 PF 18-APR-2001; 2001US-00836353.
 PR 28-OCT-1998; 98US-0105971P.
 PR 27-OCT-1999; 99WO-US025031.
 PR 19-APR-2000; 2000US-0198407P.
 XX
 PA (NIJ/J) NI J.
 PA (YOUNG) YOUNG P E.
 PA (KENNY) KENNY J J.
 PA (OLSEN) OLSEN H S.
 PA (MOORE) MOORE P A.
 PA (WEI) WEI Y.
 PA (GREENE) GREENE J M.
 PA (RUBEN) RUBEN S M.
 XX
 PI Ni J, Young PE, Kenny JJ, Olsen HS, Moore PA, Wei Y, Greene JM;
 PI Ruben SM;
 XX
 DR WPI; 2004-020335/02.
 XX
 PT New nucleic acid molecule, useful for preparing a medicament for
 PT preventing, treating or ameliorating a medical condition e.g. cancer,
 PT liver disorders or neural disorders.
 XX
 PS Disclosure; SEQ ID NO 136; 380pp; English.
 XX
 CC The invention relates to an isolated nucleic acid sequence, or its
 CC allelic variant, a fragment of the cDNA sequence, or its fragment,
 CC domain, epitope or species homologue. The nucleic acid is useful for
 CC preparing a medicament for preventing, treating or ameliorating a medical
 CC condition e.g., cancer, liver disorders such as hepatitis or neural
 CC disorders such as Alzheimer's disease. The present sequence represents
 CC the amino acid sequence of a novel human secreted protein associated
 CC protein.
 XX
 SQ Sequence 442 AA;

Query Match 100.0%; Score 2283; DB 8; Length 442;
 Best Local Similarity 100.0%; Pred. No. 5.8e-158;

Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MASVLPSSGQCAAAAAAAPPGLRRLRLLLIFSAALIPEDGQNLFTKDYTVIEGEVA 60
 DB 1 MASVLPSSGQCAAAAAAAPPGLRRLRLLLIFSAALIPEDGQNLFTKDYTVIEGEVA 60
 QY 61 TISQVNRKSDSDSVIQLNPNRQTYRPRPKDSRFQNLNSSSLKYSLTNVSISDEG 120
 DB 61 TISQVNRKSDSDSVIQLNPNRQTYRPRPKDSRFQNLNSSSLKYSLTNVSISDEG 120
 QY 121 RYFCQLYTDPPQESYTTITVLVPPNLMIDIKDTAVEGEIEIVNCTAASKPATIRWF 180
 DB 121 RYFCQLYTDPPQESYTTITVLVPPNLMIDIKDTAVEGEIEIVNCTAASKPATIRWF 180
 QY 181 KGNTELGKSEVEEMSDMTVTSQLKVKHEDDGPVLCQVEHPAVGNLTQRYLEVO 240
 DB 181 KGNTELGKSEVEEMSDMTVTSQLKVKHEDDGPVLCQVEHPAVGNLTQRYLEVO 240
 QY 241 YKPOVHIQMTYPLQGLTREGDALBELTCEAIKGPQPMVMTWVVDDEMPQHAVLSGPNLFI 300
 DB 241 YKPOVHIQMTYPLQGLTREGDALBELTCEAIKGPQPMVMTWVVDDEMPQHAVLSGPNLFI 300
 QY 301 NNLNKTNDGTYRCEASNIWGKAHSDYMLVYVDPPTTTPPTTTTPTTTTTLITLITD 360
 DB 301 NNLNKTNDGTYRCEASNIWGKAHSDYMLVYVDPPTTTPPTTTTPTTTTTLITLITD 360
 QY 361 SRAGEGSIKRAVDHAVIGVAVVVFAMLCILIIIGRYFARHKGTYFTHKAGDADADA 420
 DB 361 SRAGEGSIKRAVDHAVIGVAVVVFAMLCILIIIGRYFARHKGTYFTHKAGDADADA 420
 QY 421 DTALINAEQGQNNSEKKEKYEPI 442
 DB 421 DTALINAEQGQNNSEKKEKYEPI 442

RESULT 9
 ABO07196
 ID ABO07196 standard; protein; 442 AA.
 AC ABO07196;
 XX
 DT 13-AUG-2003 (first entry)
 XX
 DE Human p53 modifying protein, SEQ ID 156.
 XX
 KM Human; p53 modifier; cytosolic; cancer; cytosolic; antiangiogenic;
 KM antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer;
 KM lung cancer; ovarian cancer; angiogenesis; cell cycle;
 KM apoptotic disorder; cell proliferation disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200299122-A1.
 XX
 PD 12-DEC-2002.
 XX
 PF 03-JUN-2002; 2002WO-US017382.
 XX
 PR 05-JUN-2001; 2001US-0296076P.
 PR 10-OCT-2001; 2001US-0328605P.
 PR 15-FEB-2002; 2002US-0357253P.
 XX
 PA (EXEL-) EXELIXIS INC.
 XX
 PI Friedman L, Plozman GD, Belvin M, Francis-Lang H, Li D, Funke RP;
 PI WPI; 2003-156859/15.
 DR N-PSDB; ACD13371.
 XX
 PT Identifying modulators of the p53 pathway for use in treating apoptotic
 PT or cell proliferation disorders, comprises screening for agents that
 PT modulate activity of a human ortholog of genes that modify the p53
 PT pathway in Drosophila.

XX Example 2; Page 469-470; 678bp; English.
PS The invention relates to identifying (M1) a candidate p53 pathway
CC modulating agent, by contacting an assay system comprising a purified HM
CC polypeptide (human orthologue of genes that modify the p53 pathway in
CC Drosophila) or nucleic acid with a test agent under conditions, where but
CC for the presence of the test agent, the system provides a reference
CC activity, and detecting a test agent-biased activity of the assay system.
CC Also included are modulating (M2) a p53 pathway of a cell (comprising
CC contacting a cell defective in p53 function with a candidate modulator
CC that specifically binds to a HM polypeptide comprising an HM amino acid
CC sequence, where p53 function is restored), modulating (M3) a p53 pathway
CC in a mammalian cell (comprising contacting the cell with an agent that
CC specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4)
CC a disease in a patient (comprising: (a) obtaining a biological sample
CC from the patient; (b) contacting the sample with a probe for HM
CC expression; (c) comparing the results with a control; and (d) determining
CC whether the comparison indicates a likelihood disease). (M1) is useful
CC for identifying modulators of the p53 pathway. A probe for HM expression
CC is useful for diagnosing breast, colon, kidney, lung and ovarian cancer,
CC in a patient, where the cancer has greater than 25 % expression level.
CC Modulators identified by (M1) are useful in a variety of diagnostic and
CC therapeutic applications, where disease or disorder prognosis is related
CC to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell
CC proliferation disorders (e.g. cancer). Another two new methods (M2 and
CC M3) are useful for modulating the p53 pathway of a cell, thus restoring
CC the p53 function of the cell, so that the cell undergoes normal
CC proliferation or progression through the cell cycle. (M2) and (M3) are
CC also useful for treating defects in the p53 pathway such as angiogenic,
CC apoptotic or cell proliferation disorders. The present sequence
CC represents a human p53 pathway modifying protein
CC
XX Sequence 442 AA:
SQ
Query Match 99.9%; Score 2280; DB 6; Length 442;
Best Local Similarity 99.8%; Pred. No. 9.6e-158;
Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MASVVLPSGSGCAAAAAAAPPGLRLRLLLLSAALLPTGGQNLFTKQTVLIGEVA 60
DB 1 MASVVLPSGSGCAAAAAAAPPGLRLRLLLLSAALLPTGGQNLFTKQTVLIGEVA 60
QY 61 TISQVKKSDSVOLNPNKQTYFRDPRLKDSRQOLNFSSELKXSLTNVTSISDEG 120
DB 61 TISQVKKSDSVOLNPNKQTYFRDPRLKDSRQOLNFSSELKXSLTNVTSISDEG 120
QY 121 RYFQGLYDPPQESYTTITVLVPPRNLMDIQKDTAVEGEIEVNCATVASKPATIRMF 180
DB 121 RYFQGLYDPPQESYTTITVLVPPRNLMDIQKDTAVEGEIEVNCATVASKPATIRMF 180
QY 181 KGNTELKKSSEVEMSDMYTTSQMLKVKHEDGVICQVHPATNGLQRYLVEVG 240
DB 181 KGNTELKKSSEVEMSDMYTTSQMLKVKHEDGVICQVHPATNGLQRYLVEVG 240
QY 181 KGNTELKKSSEVEMSDMYTTSQMLKVKHEDGVICQVHPATNGLQRYLVEVG 240
DB 181 KGNTELKKSSEVEMSDMYTTSQMLKVKHEDGVICQVHPATNGLQRYLVEVG 240
QY 241 YKPCVHIQMTYPLQGLTFREGDALTECEATGKPPQVWTVWVVDDEMPQAVVLSGPNLFI 300
DB 241 YKPCVHIQMTYPLQGLTFREGDALTECEATGKPPQVWTVWVVDDEMPQAVVLSGPNLFI 300
QY 301 NNKLKTDNGYTRGCAASNIVGASHSDYMLYYDPTTTPPTTTTTTTTTTTTTTTTT 360
DB 301 NNKLKTDNGYTRGCAASNIVGASHSDYMLYYDPTTTPPTTTTTTTTTTTTTTTTT 360
QY 361 SRAGEGSRIVADAVVAGVAVVFMALCLLILIGRYFARHKQTYFTHEAKGADDAADA 420
DB 361 SRAGEGSRIVADAVVAGVAVVFMALCLLILIGRYFARHKQTYFTHEAKGADDAADA 420
QY 421 DTATINAEQGNNSSEKKKEYFI 442
DB 421 DTATINAEQGNNSSEKKKEYFI 442

RESULT 10

AB007231
ID AB007231 standard; protein; 442 AA.
XX
AC AB007231;
XX
DT 13-AUG-2003 (first entry)
XX
DE Human p53 modifying protein, SEQ ID 191.
XX
KM Human; p53 modifier; cytosolic; cancer; cytostatic; antiangiogenic;
KM antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer;
KM lung cancer; ovarian cancer; angiogenesis; cell cycle;
KM apoptotic disorder; cell proliferation disorder.
XX
OS Homo sapiens.
XX
PN WO200299122-A1.
XX
PD 12-DEC-2002.
XX
PF 03-JUN-2002; 2002WO-US017382.
XX
PR 05-JUN-2001; 2001US-0296076P.
PR 10-OCT-2001; 2001US-0328605P.
PR 15-FEB-2002; 2002US-0357253P.
XX
PA (EXEL-) EXELIXIS INC.
XX
PI Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;
XX
XX MPI: 2003-156859/15.
DR N-PSDB; ACD13404.
XX
DR
XX
PT Identifying modulators of the p53 pathway for use in treating apoptotic
PT or cell proliferation disorders, comprises screening for agents that
PT modulate activity of a human ortholog of genes that modify the p53
PT pathway in Drosophila.
XX
PS Example 2; Page 557-559; 678bp; English.
XX
CC The invention relates to identifying (M1) a candidate p53 pathway
CC modulating agent, by contacting an assay system comprising a purified HM
CC polypeptide (human orthologue of genes that modify the p53 pathway in
CC Drosophila) or nucleic acid with a test agent under conditions, where but
CC for the presence of the test agent, the system provides a reference
CC activity, and detecting a test agent-biased activity of the assay system.
CC Also included are modulating (M2) a p53 pathway of a cell (comprising
CC contacting a cell defective in p53 function with a candidate modulator
CC that specifically binds to a HM polypeptide comprising an HM amino acid
CC sequence, where p53 function is restored), modulating (M3) a p53 pathway
CC in a mammalian cell (comprising contacting the cell with an agent that
CC specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4)
CC a disease in a patient (comprising: (a) obtaining a biological sample
CC from the patient; (b) contacting the sample with a probe for HM
CC expression; (c) comparing the results with a control; and (d) determining
CC whether the comparison indicates a likelihood disease). (M1) is useful
CC for identifying modulators of the p53 pathway. A probe for HM expression
CC is useful for diagnosing breast, colon, kidney, lung and ovarian cancer,
CC in a patient, where the cancer has greater than 25 % expression level.
CC Modulators identified by (M1) are useful in a variety of diagnostic and
CC therapeutic applications, where disease or disorder prognosis is related
CC to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell
CC proliferation disorders (e.g. cancer). Another two new methods (M2 and
CC M3) are useful for modulating the p53 pathway of a cell, thus restoring
CC the p53 function of the cell, so that the cell undergoes normal
CC proliferation or progression through the cell cycle. (M2) and (M3) are
CC also useful for treating defects in the p53 pathway such as angiogenic,
CC apoptotic or cell proliferation disorders. The present sequence
CC represents a human p53 pathway modifying protein
CC
SQ Sequence 442 AA:
Query Match 99.9%; Score 2280; DB 6; Length 442;

Best Local Similarity 99.8%; Pred. No. 9.6e-158;
Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MASVLPSSGSCCAAAAAAAPPGLRLRLLLFSAALIPDQGNLFKDTVTYIEGEVA 60
DB 1 MASVLPSSGSCCAAAAAAAPPGLRLRLLLFSAALIPDQGNLFKDTVTYIEGEVA 60
QY 61 TISQVKNKSDSDSVIQLNPNRQTIYFRDPRPLKDSRFQLNFSSELKVSILNVSISDEG 120
DB 61 TISQVKNKSDSDSVIQLNPNRQTIYFRDPRPLKDSRFQLNFSSELKVSILNVSISDEG 120
QY 121 RYFCOLYTDPPQESYTTITVLPVPRNLMIDICKOTAVGESEIEVNCTMAASKPATITRMF 180
DB 121 RYFCOLYTDPPQESYTTITVLPVPRNLMIDICKOTAVGESEIEVNCTMAASKPATITRMF 180
QY 181 KGNTELKGSSEVEEMSDMYTTSQMLKVKHEDDGVPIQVEHPATVGNLQTORYLEVQ 240
DB 181 KGNTELKGSSEVEEMSDMYTTSQMLKVKHEDDGVPIQVEHPATVGNLQTORYLEVQ 240
QY 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKPOVMTVWVRVDEMPQHAVLSGPNLFI 300
DB 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKPOVMTVWVRVDEMPQHAVLSGPNLFI 300
QY 301 NNLNKTDNGTYRCEASNIWGAHSDYMLVYDPTTIPPTTTTTTTTTTTTTTTTTTTTT 360
DB 301 NNLNKTDNGTYRCEASNIWGAHSDYMLVYDPTTIPPTTTTTTTTTTTTTTTTTTTTT 360
QY 361 SRAGEGSIKRAVDHAVIGVAVVVFAMLCILIIIGRYFARHKGTYFTEAKGADDAADA 420
DB 361 SRAGEGSIKRAVDHAVIGVAVVVFAMLCILIIIGRYFARHKGTYFTEAKGADDAADA 420
QY 421 DTATINAGGQNNSEKKEYFI 442
DB 421 DTATINAGGQNNSEKKEYFI 442

RESULT 11
ADE61605
ID ADE61605 standard; protein; 442 AA.
XX
AC ADE61605;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein AAF69029, SEQ ID NO 7525.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SN1; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; AAF69029.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX

```

PS Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SN1)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

SO Sequence 442 AA:

Query Match 99.9%; Score 2280; DB 7; Length 442;
Best Local Similarity 99.8%; Pred. No. 9.6e-158;
Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MASVLPSSGSCCAAAAAAAPPGLRLRLLLFSAALIPDQGNLFKDTVTYIEGEVA 60
DB 1 MASVLPSSGSCCAAAAAAAPPGLRLRLLLFSAALIPDQGNLFKDTVTYIEGEVA 60
QY 61 TISQVKNKSDSDSVIQLNPNRQTIYFRDPRPLKDSRFQLNFSSELKVSILNVSISDEG 120
DB 61 TISQVKNKSDSDSVIQLNPNRQTIYFRDPRPLKDSRFQLNFSSELKVSILNVSISDEG 120
QY 121 RYFCOLYTDPPQESYTTITVLPVPRNLMIDICKOTAVGESEIEVNCTMAASKPATITRMF 180
DB 121 RYFCOLYTDPPQESYTTITVLPVPRNLMIDICKOTAVGESEIEVNCTMAASKPATITRMF 180
QY 181 KGNTELKGSSEVEEMSDMYTTSQMLKVKHEDDGVPIQVEHPATVGNLQTORYLEVQ 240
DB 181 KGNTELKGSSEVEEMSDMYTTSQMLKVKHEDDGVPIQVEHPATVGNLQTORYLEVQ 240
QY 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKPOVMTVWVRVDEMPQHAVLSGPNLFI 300
DB 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKPOVMTVWVRVDEMPQHAVLSGPNLFI 300
QY 301 NNLNKTDNGTYRCEASNIWGAHSDYMLVYDPTTIPPTTTTTTTTTTTTTTTTTTTTT 360
DB 301 NNLNKTDNGTYRCEASNIWGAHSDYMLVYDPTTIPPTTTTTTTTTTTTTTTTTTTTT 360
QY 361 SRAGEGSIKRAVDHAVIGVAVVVFAMLCILIIIGRYFARHKGTYFTEAKGADDAADA 420
DB 361 SRAGEGSIKRAVDHAVIGVAVVVFAMLCILIIIGRYFARHKGTYFTEAKGADDAADA 420
QY 421 DTATINAGGQNNSEKKEYFI 442
DB 421 DTATINAGGQNNSEKKEYFI 442

RESULT 12
ADE61608
ID ADE61608 standard; protein; 442 AA.
XX

```

AC ADE61608;
XX 29-JAN-2004 (first entry)
XX
XX Human Protein AAF69029, SEQ ID NO 7528.
DE
XX Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KM spared nerve injury; SNI; Chung.
XX Homo sapiens.
OS
XX MO2003016475-A2.
FN
XX 27-FEB-2003.
PD
XX 14-AUG-2002; 2002WO-US025765.
FF
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GENO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
PI WPI; 2003-268312/26.
XX GENBANK; AAF69029.
DR
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
FT
XX Claim 1; Page: 1017P; English.
PS
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pcr_sequences.
CC
XX Sequence 442 AA;
SQ

Query Match 99.9%; Score 2280; DB 7; Length 442;
Best Local Similarity 99.8%; Pred. No. 9.6e-158;
Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASVLTSGSCCAAAAAAPGRLRLILFFAALITPGGONLFTKDVIVIGGEVA 60
DB 1 MASVLTSGSCCAAAAAAPGRLRLILFFAALITPGGONLFTKDVIVIGGEVA 60

QY 61 TISGVNKSDDSVIQLNPNRQTIYFPRDLKDSRFQNLNFSSEELKVSITNVSISDEG 120
DB 61 TISGVNKSDDSVIQLNPNRQTIYFPRDLKDSRFQNLNFSSEELKVSITNVSISDEG 120
QY 121 RYFCQLYTDPPOESYTTITVLVPPRNLIMIDIQKDTAVEGEEIEVNCCTAMASKPATTRWF 180
DB 121 RYFCQLYTDPPOESYTTITVLVPPRNLIMIDIQKDTAVEGEEIEVNCCTAMASKPATTRWF 180
QY 181 KGNTELRKSEVEESDMVYTSQMLKVKHEDDGVVTCOVERPATVGNLQTORIYEVQ 240
DB 181 KGNTELRKSEVEESDMVYTSQMLKVKHEDDGVVTCOVERPATVGNLQTORIYEVQ 240
QY 241 YKPQVHIQMTYPLQGLTREGDALELTCEAIKQPQPMVTVWVVDDEMPQHAVISGPNLFI 300
DB 241 YKPQVHIQMTYPLQGLTREGDALELTCEAIKQPQPMVTVWVVDDEMPQHAVISGPNLFI 300
QY 301 NNLKNTDNGTYRCESNIVGKASDYMIVYVDPPTTIPPTTTTTTTTTTTTTTTTTTTTT 360
DB 301 NNLKNTDNGTYRCESNIVGKASDYMIVYVDPPTTIPPTTTTTTTTTTTTTTTTTTTTT 360
QY 361 SRAGEGSIKRAVDHAVIGVAVVVFAMLCLLILGRYFARKGTFTHEAKGADADADA 420
DB 361 SRAGEGSIKRAVDHAVIGVAVVVFAMLCLLILGRYFARKGTFTHEAKGADADADA 420
QY 421 DTALINAGCGQNSEKKKEFYI 442
DB 421 DTALINAGCGQNSEKKKEFYI 442
RESULT 13
AA17830
ID AA17830 standard; protein; 440 AA.
XX
XX AA17830;
AC
XX
XX 12-AUG-1999 (first entry)
DT
XX
XX Human PRO355 protein sequence.
DE
XX Human; PRO protein; tumour necrosis factor family; TNF; cytokine;
KW secreted protein; transmembrane protein; inflammation disorder.
XX
XX Homo sapiens.
OS
XX
XX WO9928462-A2.
PN
XX 10-JUN-1999.
PD
XX
XX 01-DEC-1998; 98WO-US025108.
PF
XX
XX 03-DEC-1997; 97US-0067411P. PRO 243
PR 11-DEC-1997; 97US-0068278P. PRO 244
PR 11-DEC-1997; 97US-0068333P. PRO 249
PR 11-DEC-1997; 97US-0069335P. PRO 249
PR 12-DEC-1997; 97US-0069425P. PRO 249
PR 16-DEC-1997; 97US-0069694P. PRO 249
PR 16-DEC-1997; 97US-0069696P. PRO 249
PR 16-DEC-1997; 97US-0069702P. PRO 249
PR 17-DEC-1997; 97US-0069870P. PRO 249
PR 17-DEC-1997; 97US-0069872P. PRO 249
PR 18-DEC-1997; 97US-0068017P. PRO 249
PR 05-JAN-1998; 98US-0070440P. PRO 249
PR 09-FEB-1998; 98US-0074086P. PRO 249
PR 09-FEB-1998; 98US-0074092P. PRO 249
PR 25-FEB-1998; 98US-0075945P. PRO 249
XX
XX (GENO) GENENTECH INC.
PA
XX Wood WJ, Goddard A, Gurney AL, Yuan J, Baker KP, Chen J;
PI WPI; 1999-37118/31.
XX N-PSDB; AAX80055.
DR
XX

PT Nucleic acids encoding PRO secreted and transmembrane proteins.

XX Claim 12; Fig 27; 13pp; English.

XX The present invention describes nucleic acids encoding PRO secreted and transmembrane proteins used therapeutically. The PRO proteins have cytosolic, anti-inflammatory, anti-proliferative and immunosuppressive activity. The proteins and polynucleotides can be used in therapy identification of homologues, raising antibodies and design of probes and primers. They can be used in a range of diseases related to proteins that they have homology with, e.g. a PRO protein having homology to complement proteins may be used in inflammatory responses

XX Sequence 440 AA;

Query Match 99.1%; Score 2263; DB 2; Length 440;
Best Local Similarity 99.5%; Fred. No. 1.7e-156;
Matches 440; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

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DB 59 TISQVMSKSDSVIQLNPNRQTYFRDPRPKDSRFQNLNFSSELKVSITNVSISDEG 118
QY 121 RYFCOLYDPPROESTTTTTPVPPNLMIDIQKTAVERGEIEVNTACTAMASKPATIRWF 180
DB 119 RYFCOLYDPPROESTTTTTPVPPNLMIDIQKTAVERGEIEVNTACTAMASKPATIRWF 178
QY 181 KGNTELKSKSEVEEMSDVITVTSQMLKVKHEDDGPVTCQEHPAVTGNLQTRYLEVQ 240
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DB 299 NNLNKTDNGTYRCESASNVGKAHSDVMLVYDPTTTPPTTTTTTTTTTTTTTTTT 358
QY 361 SRAGEGSGIRAVDAVIGVAVVVFAMLCIIILGRYFAHKGTYTTHKAGDADADA 420
DB 359 SRAGEGSGIRAVDAVIGVAVVVFAMLCIIILGRYFAHKGTYTTHKAGDADADA 418
QY 421 DTAINAEGGQNNSEKKEFYI 442
DB 419 DTAINAEGGQNNSEKKEFYI 440

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RESULT 14
AAB01321
ID AAB01321 standard; protein; 440 AA.

XX AAB01321;

XX 25-SEP-2000 (first entry)

XX Human PRO355 polypeptide.

XX PRO; membrane bound protein; secreted protein; PRO357; PRO327; PRO243;
XX PRO715; PRO241; PRO323; PRO299; PRO323; PRO344; PRO355; PRO353;
XX PRO361; PRO365; transmembrane polypeptide; antibody; screening;
XX detection; inhibition; probe; primer; human.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 1..36

XX Modified-site 9..15
FT label= Signal peptide

```

FT Modified-site /note="N-myristoylation site"
FT Modified-site 65..69
FT Modified-site /note="N-glycosylation site"
FT Modified-site 99..103
FT Modified-site /note="N-glycosylation site"
FT Modified-site 111..115
FT Modified-site /note="N-glycosylation site"
FT Modified-site 163..167
FT Modified-site /note="N-glycosylation site"
FT Modified-site 227..233
FT Modified-site /note="N-myristoylation site"
FT Modified-site 233..240
FT Modified-site /note="Tyrosine kinase phosphorylation site"
FT Modified-site 302..306
FT Modified-site /note="N-glycosylation site"
FT Modified-site 306..310
FT Modified-site /note="N-glycosylation site"
FT Modified-site 307..313
FT Modified-site /note="N-myristoylation site"
FT Modified-site 319..328
FT Modified-site /note="Tyrosine kinase phosphorylation site"
FT Modified-site 355..371
FT Modified-site /note="N-myristoylation site"
FT Domain 372..393
FT Modified-site /label="Transmembrane domain"
FT Modified-site 376..382
FT Modified-site /note="N-myristoylation site"
FT Modified-site 402..408
FT Modified-site /note="N-myristoylation site"
FT Modified-site 411..417
FT Modified-site /note="N-myristoylation site"
FT Modified-site 427..433
FT Modified-site /note="N-myristoylation site"
FT Modified-site 428..432
FT Modified-site /note="N-myristoylation site"
FT Modified-site 430..434
FT Modified-site /note="N-glycosylation site"
XX MO200032776-A2.
XX 08-JUN-2000.
XX PF 01-DEC-1999; 99WO-US028301.
XX PF 01-DEC-1998; 98WO-US025108.
XX PR 16-DEC-1998; 98US-0112850P.
XX PR 22-DEC-1998; 98US-0113296P.
XX PA (GETH ) GENENTECH INC.
XX Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E,
XX Gerlitsen ME, Goddard A, Godowski PJ, Grimaldi CU, Gueney AL,
XX Hillan KJ, Kijavlin IU, Napier MA, Roy MA, Tumas D, Wood WI;
XX WPI; 2000-412324/35.
XX DR N-PSDB; AAA95563.
XX PF New human nucleic acids encoding secreted and transmembrane polypeptides,
XX PT designated as PRO polypeptides, useful as pharmaceutical and diagnostic
XX PT agents.
XX Claim 12; Fig 24; 187pp; English.
XX New human nucleic acids encoding secreted and transmembrane polypeptides
XX which are designated as PRO polypeptides are described. The membrane-bound
XX proteins have various industrial applications, including as
XX pharmaceutical and diagnostic agents. The membrane-bound proteins can
XX also be employed for screening of potential peptide or small molecule
XX inhibitors of the relevant receptor/ligand interaction. Anti-PRO
XX antibodies are useful for the affinity purification of PRO from
XX recombinant cell culture or natural sources
XX Sequence 440 AA;
SQ

```

Query Match 99.1%; Score 2263; DB 3; Length 440;
 Best Local Similarity 99.5%; Pred. No. 1.7e-156;
 Matches 440; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 MASVVLPSGSCCAAAAAAPGRLRLRLLLLFSAALIFPTGQONLFTKDVYIEGEVA 60
 DB 1 MASVVLPSGSCCAAAAAAPG--LRLLLLFSAALIFPTGQONLFTKDVYIEGEVA 58
 QY 61 TISCQVNSDSDSVIQLNPNRQTIYFRDPRFKDSRFQLNFSSELKVSILTVNISDEG 120
 DB 59 TISCQVNSDSDSVIQLNPNRQTIYFRDPRFKDSRFQLNFSSELKVSILTVNISDEG 118
 QY 121 RYFCQLYTDPQESYTTITVLVPRNLMIDIQKDTAVEGEIEVNCATMAKSPATTIRMF 180
 DB 119 RYFCQLYTDPQESYTTITVLVPRNLMIDIQKDTAVEGEIEVNCATMAKSPATTIRMF 178
 QY 181 KGNTELKGSKEVSEWSDMTYTTISQMLKVKHEKDGAVVICOVHPANTGMLQORILEVQ 240
 DB 179 KGNTELKGSKEVSEWSDMTYTTISQMLKVKHEKDGAVVICOVHPANTGMLQORILEVQ 238
 QY 241 YKPOVHICMTYPLGLTREGDALTECEALGKPPQVAVTVWVDEMPQAVLSGNLFI 300
 DB 239 YKPOVHICMTYPLGLTREGDALTECEALGKPPQVAVTVWVDEMPQAVLSGNLFI 298
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 DB 299 NNLNKTDNGYRCASINIVGKASDVMLYYDPTTIPPTTTTTTTTTTTTTTTTT 358
 QY 361 SRAGEGSIKAVDAVAVGVAVVFMCLLILGRIYFARHGKTYTHAKGADDAADA 420
 DB 359 SRAGEGSIKAVDAVAVGVAVVFMCLLILGRIYFARHGKTYTHAKGADDAADA 418
 QY 421 DTATINAEQGQNNSEKKEYFI 442
 DB 419 DTATINAEQGQNNSEKKEYFI 440

RESULT 15
 AAU29040
 ID AAU29040 standard; protein; 440 AA.
 AC AAU29040;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DB Human PRO polypeptide sequence #17.
 XX
 KW PRO polypeptide; mammary; tumour; cancer; human; cattle; horse; sheep;
 KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO20016848-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 28-FEB-2001; 2001WO-US006530.
 XX
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 03-MAR-2000; 2000US-018702P.
 PR 06-MAR-2000; 2000US-0186968P.
 PR 14-MAR-2000; 2000US-0189320P.
 PR 14-MAR-2000; 2000US-0189328P.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 21-MAR-2000; 2000US-0190828P.
 PR 21-MAR-2000; 2000US-0191007P.
 PR 21-MAR-2000; 2000US-0191048P.
 PR 21-MAR-2000; 2000US-0191314P.
 PR 28-MAR-2000; 2000US-0192655P.

PR 29-MAR-2000; 2000US-0193032P.
 PR 29-MAR-2000; 2000US-0193053P.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 04-APR-2000; 2000US-0194449P.
 PR 04-APR-2000; 2000US-0194647P.
 PR 11-APR-2000; 2000US-0195975P.
 PR 11-APR-2000; 2000US-0196000P.
 PR 11-APR-2000; 2000US-0196187P.
 PR 11-APR-2000; 2000US-0196690P.
 PR 11-APR-2000; 2000US-0196820P.
 PR 18-APR-2000; 2000US-0198121P.
 PR 18-APR-2000; 2000US-0198585P.
 PR 25-APR-2000; 2000US-0199397P.
 PR 25-APR-2000; 2000US-0199550P.
 PR 25-APR-2000; 2000US-0199654P.
 PR 03-MAY-2000; 2000US-0201516P.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 22-AUG-2000; 2000US-00644848.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000WO-US034956.
 PA (GENTH) GENENTECH INC.
 XX
 PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 PI Pan U, Smith V, Watanabe CK, Wood WI, Zhang Z;
 DR WPI; 2001-602746/68.
 DR N-PSDB; AAS45941.
 XX
 PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the
 PT presence of tumors, such as prostate and breast tumors, in mammals and to
 PT screen for modulators of the compounds.
 XX
 PS Claim 11; Fig 34; 774pp; English.
 XX
 CC Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
 CC The PRO polypeptides and their associated nucleic acids can be used to
 CC detect the presence of a tumour in a mammal by comparing the level of
 CC expression of a PRO polypeptide in a test sample of cells from the animal
 CC and a control sample of normal cells, whereby a higher level of
 CC expression in the test sample indicates the presence of a tumour in the
 CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
 CC and rabbits but are preferably human. The polypeptides can be used to
 CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
 CC when contacted with it. A specific polypeptide can be used to stimulate
 CC the proliferation or differentiation of chondrocyte cells. The PRO
 CC proteins can be used to determine the presence of tumours and also
 CC susceptibility to tumour development, particularly adrenal, lung, colon,
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
 CC can be used for genetic analysis of individuals with genetic disorders
 XX

SO Sequence 440 AA:
 Query Match 99.1%; Score 2263; DB 4; Length 440;
 Best Local Similarity 99.5%; Pred. No. 1.7e-156;
 Matches 440; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 MASVVLPSGSCCAAAAAAPGRLRLRLLLLFSAALIFPTGQONLFTKDVYIEGEVA 60
 DB 1 MASVVLPSGSCCAAAAAAPG--LRLLLLFSAALIFPTGQONLFTKDVYIEGEVA 58
 QY 61 TISCQVNSDSDSVIQLNPNRQTIYFRDPRFKDSRFQLNFSSELKVSILTVNISDEG 120
 DB 59 TISCQVNSDSDSVIQLNPNRQTIYFRDPRFKDSRFQLNFSSELKVSILTVNISDEG 118

QY 121 RYFCQLYTDPPOESYTTITVLVPPRNLMIDIQKDTAVEGEIEVNTCTANASKPATITRMF 180
Db 119 RYFCQLYTDPPOESYTTITVLVPPRNLMIDIQKDTAVEGEIEVNTCTANASKPATITRMF 178
QY 181 KGNTEILKKSSEVEWSDMYTTSQMLKXHKEDDGVVICQVEHPATGNLQTORYLEVQ 240
Db 179 KGNTEILKKSSEVEWSDMYTTSQMLKXHKEDDGVVICQVEHPATGNLQTORYLEVQ 238
QY 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKPOVNVWTVRVYDDEMPCHAVLSGPYLF 300
Db 239 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKPOVNVWTVRVYDDEMPCHAVLSGPYLF 298
QY 301 NNLNKTNDNGTYRCASNIYVKAHSDYMLYYDPPTTTPPTTTTTTTTTTTTTTTTT 360
Db 299 NNLNKTNDNGTYRCASNIYVKAHSDYMLYYDPPTTTPPTTTTTTTTTTTTTTTTT 358
QY 361 SRAGEGSIKRAVDHAVIGVAVVVFAMLCLLILGRYFARHKGTFTHEAKGADDAADA 420
Db 359 SRAGEGSIKRAVDHAVIGVAVVVFAMLCLLILGRYFARHKGTFTHEAKGADDAADA 418
QY 421 DTALINAEAGGONNSEKKEKYPFI 442
Db 419 DTALINAEAGGONNSEKKEKYPFI 440

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Job time : 83.6694 secs

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DB 181 KGNTELKKGSEVEEMSDMTVTLSQMLKVHKKEDDGVPIYCOVEHPAVTGNLQOTORYLEVO 240
QY 241 YKPOVHIOMTYPLQGLTREGDALELTCEAIKGPQVWVTVWRVDEMPQAHVLSGPNLFI 300
DB 241 YKPOVHIOMTYPLQGLTREGDALELTCEAIKGPQVWVTVWRVDEMPQAHVLSGPNLFI 300
QY 301 NNUNKTNDNGTYRCESASNVGKAHSDYMLVYVDPPTTTPPTTTTTTTTTTTTTTTTTTTTT 360
DB 301 NNUNKTNDNGTYRCESASNVGKAHSDYMLVYVDPPTTTPPTTTTTTTTTTTTTTTTTTTTT 360
QY 361 SRAGEGSIKRAVDHVAIGVAVVVFAMLCIIILIGRYFARHKGTYFTHKAGADDAADA 420
DB 361 SRAGEGSIKRAVDHVAIGVAVVVFAMLCIIILIGRYFARHKGTYFTHKAGADDAADA 420
QY 421 DTAIINAEAGGONNSEKKEEYFI 442
DB 421 DTAIINAEAGGONNSEKKEEYFI 442

RESULT 2

US-09-778-187B-2
; Sequence 2, Application US/09778187B
; Patent No. US20020168712A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Farnlow III, William C
; TITLE OF INVENTION: MOLECULES DESIGNATED LDCAV
; FILE REFERENCE: 2873-US
; CURRENT APPLICATION NUMBER: US/09/778,187B
; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: PCT/US99/17905
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: US 60/095,672
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 442
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-778-187B-2

Query Match 100.0%; Score 2283; DB 9; Length 442;
Best Local Similarity 100.0%; Pred. No. 9.1e-177;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASVVLPSGSCCAAAAAAAPPGLRLRLLLLFSAALIPFGDQNLFTKDVTVIEGEVA 60
DB 1 MASVVLPSGSCCAAAAAAAPPGLRLRLLLLFSAALIPFGDQNLFTKDVTVIEGEVA 60
QY 61 TISQVNSKSDSVIQLNPNKQTIYFRDFRPLKDSRFQOLNFSSELKVSILTVNISIDEG 120
DB 61 TISQVNSKSDSVIQLNPNKQTIYFRDFRPLKDSRFQOLNFSSELKVSILTVNISIDEG 120
QY 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGSEIEVNCTAMASKPATITIRMF 180
DB 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGSEIEVNCTAMASKPATITIRMF 180
QY 181 KGNTELKKGSEVEEMSDMTVTLSQMLKVHKKEDDGVPIYCOVEHPAVTGNLQOTORYLEVO 240
DB 181 KGNTELKKGSEVEEMSDMTVTLSQMLKVHKKEDDGVPIYCOVEHPAVTGNLQOTORYLEVO 240
QY 241 YKPOVHIOMTYPLQGLTREGDALELTCEAIKGPQVWVTVWRVDEMPQAHVLSGPNLFI 300
DB 241 YKPOVHIOMTYPLQGLTREGDALELTCEAIKGPQVWVTVWRVDEMPQAHVLSGPNLFI 300
QY 301 NNUNKTNDNGTYRCESASNVGKAHSDYMLVYVDPPTTTPPTTTTTTTTTTTTTTTTTTTTT 360
DB 301 NNUNKTNDNGTYRCESASNVGKAHSDYMLVYVDPPTTTPPTTTTTTTTTTTTTTTTTTTTT 360
QY 361 SRAGEGSIKRAVDHVAIGVAVVVFAMLCIIILIGRYFARHKGTYFTHKAGADDAADA 420
DB 361 SRAGEGSIKRAVDHVAIGVAVVVFAMLCIIILIGRYFARHKGTYFTHKAGADDAADA 420

DB 361 SRAGEGSIKRAVDHVAIGVAVVVFAMLCIIILIGRYFARHKGTYFTHKAGADDAADA 420
QY 421 DTAIINAEAGGONNSEKKEEYFI 442
DB 421 DTAIINAEAGGONNSEKKEEYFI 442

RESULT 3

US-09-984-130-136
; Sequence 136, Application US/09984130
; Publication No. US200300525231A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 12 Human Secreted Proteins
; FILE REFERENCE: P48992
; CURRENT APPLICATION NUMBER: US/09/984,130
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,792
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 09/836,353
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/198,407
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: PCT/US99/25031
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 60/105,971
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 136
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-130-136

Query Match 100.0%; Score 2283; DB 10; Length 442;
Best Local Similarity 100.0%; Pred. No. 9.1e-177;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASVVLPSGSCCAAAAAAAPPGLRLRLLLLFSAALIPFGDQNLFTKDVTVIEGEVA 60
DB 1 MASVVLPSGSCCAAAAAAAPPGLRLRLLLLFSAALIPFGDQNLFTKDVTVIEGEVA 60
QY 61 TISQVNSKSDSVIQLNPNKQTIYFRDFRPLKDSRFQOLNFSSELKVSILTVNISIDEG 120
DB 61 TISQVNSKSDSVIQLNPNKQTIYFRDFRPLKDSRFQOLNFSSELKVSILTVNISIDEG 120
QY 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGSEIEVNCTAMASKPATITIRMF 180
DB 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGSEIEVNCTAMASKPATITIRMF 180
QY 181 KGNTELKKGSEVEEMSDMTVTLSQMLKVHKKEDDGVPIYCOVEHPAVTGNLQOTORYLEVO 240
DB 181 KGNTELKKGSEVEEMSDMTVTLSQMLKVHKKEDDGVPIYCOVEHPAVTGNLQOTORYLEVO 240
QY 241 YKPOVHIOMTYPLQGLTREGDALELTCEAIKGPQVWVTVWRVDEMPQAHVLSGPNLFI 300
DB 241 YKPOVHIOMTYPLQGLTREGDALELTCEAIKGPQVWVTVWRVDEMPQAHVLSGPNLFI 300
QY 301 NNUNKTNDNGTYRCESASNVGKAHSDYMLVYVDPPTTTPPTTTTTTTTTTTTTTTTTTTTT 360
DB 301 NNUNKTNDNGTYRCESASNVGKAHSDYMLVYVDPPTTTPPTTTTTTTTTTTTTTTTTTTTT 360
QY 361 SRAGEGSIKRAVDHVAIGVAVVVFAMLCIIILIGRYFARHKGTYFTHKAGADDAADA 420
DB 361 SRAGEGSIKRAVDHVAIGVAVVVFAMLCIIILIGRYFARHKGTYFTHKAGADDAADA 420
QY 421 DTAIINAEAGGONNSEKKEEYFI 442
DB 421 DTAIINAEAGGONNSEKKEEYFI 442

RESULT 4

US-09-836-353A-136
 ; Sequence 136, Application US/09836353A
 ; Publication No. US20030129685A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ni et al.
 ; TITLE OF INVENTION: 12 Human Secreted Proteins
 ; FILE REFERENCE: P489P1
 ; CURRENT APPLICATION NUMBER: US/09/836,353A
 ; CURRENT FILING DATE: 2001-04-18
 ; PRIOR APPLICATION NUMBER: 60/198,407
 ; PRIOR FILING DATE: 2000-04-19
 ; PRIOR APPLICATION NUMBER: PCT/US99/25031
 ; PRIOR FILING DATE: 1999-10-27
 ; PRIOR APPLICATION NUMBER: 60/105,971
 ; PRIOR FILING DATE: 1998-10-28
 ; NUMBER OF SEQ ID NOS: 147
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 136
 ; LENGTH: 442
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-836-353A-136

Query Match 100.0%; Score 2283; DB 10; Length 442;
 Best Local Similarity 100.0%; Pred. No. 9,1e-177;
 Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASVLPSSGSCAAAAAAPPGLRLRLLLLFSAALIPFGDGNLFTKDVTVIEGEVA 60
 DB 1 MASVLPSSGSCAAAAAAPPGLRLRLLLLFSAALIPFGDGNLFTKDVTVIEGEVA 60
 QY 61 TISQVNSKSDSVIQLNPNRQTIYFRDPRPKDSRFQLNFSSELKVSILTVNISDEG 120
 DB 61 TISQVNSKSDSVIQLNPNRQTIYFRDPRPKDSRFQLNFSSELKVSILTVNISDEG 120
 QY 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEIEVNCCTAMASKPATIRMF 180
 DB 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEIEVNCCTAMASKPATIRMF 180
 QY 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEIEVNCCTAMASKPATIRMF 180
 DB 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEIEVNCCTAMASKPATIRMF 180
 QY 181 KGNTELKGSVEEEMSDMTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQTORYLEVO 240
 DB 181 KGNTELKGSVEEEMSDMTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQTORYLEVO 240
 QY 181 KGNTELKGSVEEEMSDMTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQTORYLEVO 240
 DB 181 KGNTELKGSVEEEMSDMTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQTORYLEVO 240
 QY 241 YKPOVHIQMTYPLQGLTREGDALLETCEALGKPOVMTWVRVDEMPQHAVALSGPNLFI 300
 DB 241 YKPOVHIQMTYPLQGLTREGDALLETCEALGKPOVMTWVRVDEMPQHAVALSGPNLFI 300
 QY 301 NNLNKTNGTYRCEASNIWGAHSDYMLVYDPTTIPPTTTTTTTTTTTTTTTTTTT 360
 DB 301 NNLNKTNGTYRCEASNIWGAHSDYMLVYDPTTIPPTTTTTTTTTTTTTTTTTTT 360
 QY 301 NNLNKTNGTYRCEASNIWGAHSDYMLVYDPTTIPPTTTTTTTTTTTTTTTTTTT 360
 DB 301 NNLNKTNGTYRCEASNIWGAHSDYMLVYDPTTIPPTTTTTTTTTTTTTTTTTTT 360
 QY 361 SRAGEGSIKRAVDHAVIGVAVVVFAMLCILIIIGRYFARHKGTFTHEAKGADDAADA 420
 DB 361 SRAGEGSIKRAVDHAVIGVAVVVFAMLCILIIIGRYFARHKGTFTHEAKGADDAADA 420
 QY 361 SRAGEGSIKRAVDHAVIGVAVVVFAMLCILIIIGRYFARHKGTFTHEAKGADDAADA 420
 DB 361 SRAGEGSIKRAVDHAVIGVAVVVFAMLCILIIIGRYFARHKGTFTHEAKGADDAADA 420
 QY 421 DTALINAEAGGNNSEKKEYFI 442
 DB 421 DTALINAEAGGNNSEKKEYFI 442

RESULT 5

US-10-363-616-262
 ; Sequence 262, Application US/10363616
 ; Publication No. US20040044181A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
 ; FILE REFERENCE: 21272-113 (793)
 ; CURRENT APPLICATION NUMBER: US/10/363,616
 ; CURRENT FILING DATE: 2003-03-03
 ; PRIOR APPLICATION NUMBER: 09/654,935
 ; PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 490

SEQ ID NO 262
 ; LENGTH: 442
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-363-616-262

Query Match 100.0%; Score 2283; DB 12; Length 442;
 Best Local Similarity 100.0%; Pred. No. 9,1e-177;
 Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASVLPSSGSCAAAAAAPPGLRLRLLLLFSAALIPFGDGNLFTKDVTVIEGEVA 60
 DB 1 MASVLPSSGSCAAAAAAPPGLRLRLLLLFSAALIPFGDGNLFTKDVTVIEGEVA 60
 QY 61 TISQVNSKSDSVIQLNPNRQTIYFRDPRPKDSRFQLNFSSELKVSILTVNISDEG 120
 DB 61 TISQVNSKSDSVIQLNPNRQTIYFRDPRPKDSRFQLNFSSELKVSILTVNISDEG 120
 QY 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEIEVNCCTAMASKPATIRMF 180
 DB 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEIEVNCCTAMASKPATIRMF 180
 QY 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEIEVNCCTAMASKPATIRMF 180
 DB 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEIEVNCCTAMASKPATIRMF 180
 QY 181 KGNTELKGSVEEEMSDMTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQTORYLEVO 240
 DB 181 KGNTELKGSVEEEMSDMTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQTORYLEVO 240
 QY 241 YKPOVHIQMTYPLQGLTREGDALLETCEALGKPOVMTWVRVDEMPQHAVALSGPNLFI 300
 DB 241 YKPOVHIQMTYPLQGLTREGDALLETCEALGKPOVMTWVRVDEMPQHAVALSGPNLFI 300
 QY 301 NNLNKTNGTYRCEASNIWGAHSDYMLVYDPTTIPPTTTTTTTTTTTTTTTTTTT 360
 DB 301 NNLNKTNGTYRCEASNIWGAHSDYMLVYDPTTIPPTTTTTTTTTTTTTTTTTTT 360
 QY 301 NNLNKTNGTYRCEASNIWGAHSDYMLVYDPTTIPPTTTTTTTTTTTTTTTTTTT 360
 DB 301 NNLNKTNGTYRCEASNIWGAHSDYMLVYDPTTIPPTTTTTTTTTTTTTTTTTTT 360
 QY 361 SRAGEGSIKRAVDHAVIGVAVVVFAMLCILIIIGRYFARHKGTFTHEAKGADDAADA 420
 DB 361 SRAGEGSIKRAVDHAVIGVAVVVFAMLCILIIIGRYFARHKGTFTHEAKGADDAADA 420
 QY 361 SRAGEGSIKRAVDHAVIGVAVVVFAMLCILIIIGRYFARHKGTFTHEAKGADDAADA 420
 DB 361 SRAGEGSIKRAVDHAVIGVAVVVFAMLCILIIIGRYFARHKGTFTHEAKGADDAADA 420
 QY 421 DTALINAEAGGNNSEKKEYFI 442
 DB 421 DTALINAEAGGNNSEKKEYFI 442

RESULT 6

US-10-302-041-20
 ; Sequence 20, Application US/10302041
 ; Publication No. US20030144478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baum, Peter
 ; TITLE OF INVENTION: Molecules Designated B7L1
 ; FILE REFERENCE: 2844-US
 ; CURRENT APPLICATION NUMBER: US/10/302,041
 ; CURRENT FILING DATE: 2002-11-21
 ; PRIOR APPLICATION NUMBER: US/09/778,510
 ; PRIOR FILING DATE: 2001-02-07
 ; PRIOR APPLICATION NUMBER: PCT/US99/17906
 ; PRIOR FILING DATE: 1999-08-05
 ; PRIOR APPLICATION NUMBER: 60/095,663
 ; PRIOR FILING DATE: 1998-08-07
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 20
 ; LENGTH: 442
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-10-302-041-20

Query Match 100.0%; Score 2283; DB 14; Length 442;
 Best Local Similarity 100.0%; Pred. No. 9,1e-177;
 Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASVLPSSGSCAAAAAAPPGLRLRLLLLFSAALIPFGDGNLFTKDVTVIEGEVA 60

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Db 1 MASVVLPSGSCCAAAAAAARPGRLRLLLLLLFSAALLIPTGCGQLFTKDVTVIEGEVA 60
Cy 61 TISQVKNKSDSVQLNPNKQTIYFRDFRPLKDSRFQOLNFSSELKVSILTNVISDDEG 120
Db 61 TISQVKNKSDSVQLNPNKQTIYFRDFRPLKDSRFQOLNFSSELKVSILTNVISDDEG 120
Cy 121 RYFCQLTDPQESYTTITVLVPPRNLMIDIOKDTAVEGEIEVNCNMAASKPATITIRMF 180
Db 121 RYFCQLTDPQESYTTITVLVPPRNLMIDIOKDTAVEGEIEVNCNMAASKPATITIRMF 180
Cy 181 KGNTELKGSVEEWSMVTYTSQJMLKVKHKEDDGVVICQVHPAATGNLQORYLEVQ 240
Db 181 KGNTELKGSVEEWSMVTYTSQJMLKVKHKEDDGVVICQVHPAATGNLQORYLEVQ 240
Cy 241 YKPOVHIQMTYPLQGLTRBGDALETCBAIGKPOVWVTVWRVDDEMPQAHVLSGNLFI 300
Db 241 YKPOVHIQMTYPLQGLTRBGDALETCBAIGKPOVWVTVWRVDDEMPQAHVLSGNLFI 300
Cy 301 NNLNKTNGTYRCEASNI VGRKASDYMLYVDPTTIPPTTTTTTTTTTTTTTTTTTTTT 360
Db 301 NNLNKTNGTYRCEASNI VGRKASDYMLYVDPTTIPPTTTTTTTTTTTTTTTTTTTTT 360
Cy 361 SRAGEEGSIRAVDAVAVIGVAVVAVFAMLCILIIIGRYFARHKGTYFTHAKGADDAADA 420
Db 361 SRAGEEGSIRAVDAVAVIGVAVVAVFAMLCILIIIGRYFARHKGTYFTHAKGADDAADA 420
Cy 421 DTALINAEQGQNNSEKKEVEFI 442
Db 421 DTALINAEQGQNNSEKKEVEFI 442
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RESULT 7
US-10-403-107-1

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; Sequence 1, Application US/10403107
; Publication No. US20030165974A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: REEVES, Roger
; APPLICANT: YOSHINO, Mutsuaki
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS
; FILE REFERENCE: JHU1770-1
; CURRENT APPLICATION NUMBER: US/10/403,107
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US/09/930,803
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-107-1
```

Query Match 100.0%; Score 2283; DB 14; Length 442;
Best Local Similarity 100.0%; Pred. No. 9,1e-177;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Cy 1 MASVVLPSGSCCAAAAAAARPGRLRLLLLLLFSAALLIPTGCGQLFTKDVTVIEGEVA 60
Db 1 MASVVLPSGSCCAAAAAAARPGRLRLLLLLLFSAALLIPTGCGQLFTKDVTVIEGEVA 60
Cy 61 TISQVKNKSDSVQLNPNKQTIYFRDFRPLKDSRFQOLNFSSELKVSILTNVISDDEG 120
Db 61 TISQVKNKSDSVQLNPNKQTIYFRDFRPLKDSRFQOLNFSSELKVSILTNVISDDEG 120
Cy 121 RYFCQLTDPQESYTTITVLVPPRNLMIDIOKDTAVEGEIEVNCNMAASKPATITIRMF 180
Db 121 RYFCQLTDPQESYTTITVLVPPRNLMIDIOKDTAVEGEIEVNCNMAASKPATITIRMF 180
Cy 181 KGNTELKGSVEEWSMVTYTSQJMLKVKHKEDDGVVICQVHPAATGNLQORYLEVQ 240
Db 181 KGNTELKGSVEEWSMVTYTSQJMLKVKHKEDDGVVICQVHPAATGNLQORYLEVQ 240
```

```
Cy 241 YKPOVHIQMTYPLQGLTRBGDALETCBAIGKPOVWVTVWRVDDEMPQAHVLSGNLFI 300
Db 241 YKPOVHIQMTYPLQGLTRBGDALETCBAIGKPOVWVTVWRVDDEMPQAHVLSGNLFI 300
Cy 301 NNLNKTNGTYRCEASNI VGRKASDYMLYVDPTTIPPTTTTTTTTTTTTTTTTTTTTT 360
Db 301 NNLNKTNGTYRCEASNI VGRKASDYMLYVDPTTIPPTTTTTTTTTTTTTTTTTTTTT 360
Cy 361 SRAGEEGSIRAVDAVAVIGVAVVAVFAMLCILIIIGRYFARHKGTYFTHAKGADDAADA 420
Db 361 SRAGEEGSIRAVDAVAVIGVAVVAVFAMLCILIIIGRYFARHKGTYFTHAKGADDAADA 420
Cy 421 DTALINAEQGQNNSEKKEVEFI 442
Db 421 DTALINAEQGQNNSEKKEVEFI 442
```

RESULT 8
US-10-015-115-111

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; Sequence 11, Application US/10015115
; Publication No. US20030207800A1
; GENERAL INFORMATION:
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Zetnusen, Bryan D
; APPLICANT: Patrujan, Meera
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kexuda, Ramsha
; APPLICANT: Gangoli, Bsha A
; APPLICANT: Shinkels, Richard A
; APPLICANT: Taupier, Raymond J
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralichara
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-211
; CURRENT APPLICATION NUMBER: US/10/015,115
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/248,153
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 60/249,598
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/264,240
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/266,127
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/269,562
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/304,348
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/309,261
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/313,283
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 111
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-015-115-111
```

Query Match 100.0%; Score 2283; DB 15; Length 442;
Best Local Similarity 100.0%; Pred. No. 9,1e-177;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Cy 1 MASVVLPSGSCCAAAAAAARPGRLRLLLLLLFSAALLIPTGCGQLFTKDVTVIEGEVA 60
Db 1 MASVVLPSGSCCAAAAAAARPGRLRLLLLLLFSAALLIPTGCGQLFTKDVTVIEGEVA 60
Cy 61 TISQVKNKSDSVQLNPNKQTIYFRDFRPLKDSRFQOLNFSSELKVSILTNVISDDEG 120
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Db 61 TISCQVNSDDSVIQLNPNKQTYFRDPRFKDSRFQQLNFSSELKVSLENNVSIISDEG 120
Qy 121 RYFQCLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVGEIEIVNCTAMASKPATITRMF 180
Db 121 RYFQCLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVGEIEIVNCTAMASKPATITRMF 180
Qy 181 KGNTELKGSSEVEBMSDMYTTVSQMLKVKHKEDDGVPIQVEHPAVTGNLQTOXYLEVO 240
Db 181 KGNTELKGSSEVEBMSDMYTTVSQMLKVKHKEDDGVPIQVEHPAVTGNLQTOXYLEVO 240
Qy 241 YKPOVHIQMTYPLQGLTRFGDALBELTCEAIGKPPQVMTWVRVDEMPQHAVISGPNLFI 300
Db 241 YKPOVHIQMTYPLQGLTRFGDALBELTCEAIGKPPQVMTWVRVDEMPQHAVISGPNLFI 300
Qy 301 NNLMKTDNGTYRCESASNVGKAHSDYMLVYDPTTIPPTTTTTTTTTTTTTTTTTITD 360
Db 301 NNLMKTDNGTYRCESASNVGKAHSDYMLVYDPTTIPPTTTTTTTTTTTTTTTTTITD 360
Qy 361 SRAGEEGSIRAVDHAIVGGVAVVVFAMCLIIIGRYFARHKGYTFTHAAGADDAADA 420
Db 361 SRAGEEGSIRAVDHAIVGGVAVVVFAMCLIIIGRYFARHKGYTFTHAAGADDAADA 420
Qy 421 DTALINAEQGQNNSEKKEYFI 442
Db 421 DTALINAEQGQNNSEKKEYFI 442

RESULT 9

US-10-015-115-110
; Sequence 110, Application US/10015115
; Publication No. US20030207800A1
; GENERAL INFORMATION:
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Patturajan, Meera
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesha
; APPLICANT: Gangoli, Esha A
; APPLICANT: Shinkets, Richard A
; APPLICANT: Taupier, Raymond J
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-211
; CURRENT FILING DATE: US/10/015,115
; PRIOR APPLICATION NUMBER: 60/248,153
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 60/249,598
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/264,240
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/266,127
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/269,562
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/304,348
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/309,261
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/313,283
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 110
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-015-115-110

Query Match 99.9%; Score 2280; DB 15; Length 442;
Best Local Similarity 99.8%; Pred No. 1,6e-176;
Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASVVLPSGSGQCAAAAAAAPPGLRLRLLLLSAALIPITDGGNLFRTKDYVIEGEVA 60
Db 1 MASVVLPSGSGQCAAAAAAAPPGLRLRLLLLSAALIPITDGGNLFRTKDYVIEGEVA 60
Qy 61 TISCQVNSDDSVIQLNPNKQTYFRDPRFKDSRFQQLNFSSELKVSLENNVSIISDEG 120
Db 61 TISCQVNSDDSVIQLNPNKQTYFRDPRFKDSRFQQLNFSSELKVSLENNVSIISDEG 120
Qy 121 RYFQCLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVGEIEIVNCTAMASKPATITRMF 180
Db 121 RYFQCLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVGEIEIVNCTAMASKPATITRMF 180
Qy 181 KGNTELKGSSEVEBMSDMYTTVSQMLKVKHKEDDGVPIQVEHPAVTGNLQTOXYLEVO 240
Db 181 KGNTELKGSSEVEBMSDMYTTVSQMLKVKHKEDDGVPIQVEHPAVTGNLQTOXYLEVO 240
Qy 241 YKPOVHIQMTYPLQGLTRFGDALBELTCEAIGKPPQVMTWVRVDEMPQHAVISGPNLFI 300
Db 241 YKPOVHIQMTYPLQGLTRFGDALBELTCEAIGKPPQVMTWVRVDEMPQHAVISGPNLFI 300
Qy 301 NNLMKTDNGTYRCESASNVGKAHSDYMLVYDPTTIPPTTTTTTTTTTTTTTTTTITD 360
Db 301 NNLMKTDNGTYRCESASNVGKAHSDYMLVYDPTTIPPTTTTTTTTTTTTTTTTTITD 360
Qy 361 SRAGEEGSIRAVDHAIVGGVAVVVFAMCLIIIGRYFARHKGYTFTHAAGADDAADA 420
Db 361 SRAGEEGSIRAVDHAIVGGVAVVVFAMCLIIIGRYFARHKGYTFTHAAGADDAADA 420
Qy 421 DTALINAEQGQNNSEKKEYFI 442
Db 421 DTALINAEQGQNNSEKKEYFI 442

RESULT 10

US-09-866-028-61
; Sequence 61, Application US/09866028
; Patent No. US20020058309A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Baton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerlitsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gutrey, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavlin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tomas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION data removed - consult PAM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-866-028-61

Query Match

99.1%; Score 2263; DB 9; Length 440;

Best Local Similarity 99.5%; Pred. No. 3,8e-175; Matches 440; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

CY 1 MASVLPSSGSCCAAAAAAPPGRLRLLLLSAALLPTGDCQNTFYDVVIGEVA 60
DB 1 MASVLPSSGSCCAAAAAAPPG--LRLLLLLSAALLPTGDCQNTFYDVVIGEVA 58
CY TISCVNKSDDSVQOLNPNRQTIYFRDFRPLKDSRFQOLNFSSELSKSLTVNVSISDEG 120
DB TISCVNKSDDSVQOLNPNRQTIYFRDFRPLKDSRFQOLNFSSELSKSLTVNVSISDEG 118
CY 121 RYFCQLYTDPQESYTTITVLVPPRNIMIDIQKDTAVEGEIEVNCATNASKPATITRMF 180
DB 119 RYFCQLYTDPQESYTTITVLVPPRNIMIDIQKDTAVEGEIEVNCATNASKPATITRMF 178
CY 181 KGNELKGSSEVESMSMTYTTSQMLKMHKEDDGVVICOVEHPATGLOKORYLEVG 240
DB 179 KGNELKGSSEVESMSMTYTTSQMLKMHKEDDGVVICOVEHPATGLOKORYLEVG 238
CY 241 YKPOVHQMITYPLOGLTREGDALTCEAIQKPPVWVWVVDENPQHAVLSGNPLFI 300
DB 239 YKPOVHQMITYPLOGLTREGDALTCEAIQKPPVWVWVVDENPQHAVLSGNPLFI 298
CY 301 NNLKNTDNGYTRCASNVIGKASDYMLYVDPPTTTPPTTTTTTTTTTTTTTTTTID 360
DB 299 NNLKNTDNGYTRCASNVIGKASDYMLYVDPPTTTPPTTTTTTTTTTTTTTTTTID 358
CY 361 SRAGEGSIKRAVDNAVIGVAVVVFAMLCILLIGRYFARHKGTYFTTHAKGADDAADA 420
DB 359 SRAGEGSIKRAVDNAVIGVAVVVFAMLCILLIGRYFARHKGTYFTTHAKGADDAADA 418
CY 421 DTAIINAEQGNNSSEKKEYFI 442
DB 419 DTAIINAEQGNNSSEKKEYFI 440

RESULT 11

US-09-944-449-61
Sequence 61, Application US/09944449
Patent No. US20020102647A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Bocstein, David
APPLICANT: Bacon, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gunney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kilavin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACTIS ENCODING THE SAME
FILE REFERENCE: P2348P1C1
CURRENT APPLICATION NUMBER: US/09/944,449
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425

PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,066
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020102647A1, December 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020102647A1, December 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LENGTH: 440
TYPE: PRT
ORGANISM: Homo Sapien

Query Match 99.1%; Score 2263; DB 9; Length 440;

Best Local Similarity 99.5%; Pred. No. 3.8e-175;
Matches 440; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

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QY 1 MASVLPSSGSCAAAAAAPPGLRLRLLLLFSAALITPGQONLFTKDVIVIEGEVA 60
Db 1 MASVLPSSGSCAAAAAAPPGLRLRLLLLFSAALITPGQONLFTKDVIVIEGEVA 58
QY 61 TISQVVKSDSVYQLNPNRQITFRDPRFKDSRQQLNFSSELSKSLTNVSIISDEG 120
Db 59 TISQVVKSDSVYQLNPNRQITFRDPRFKDSRQQLNFSSELSKSLTNVSIISDEG 118
QY 121 RYFQGLTDPPOESYTTITVLVPPRNIMIDIQKDTAVEGEIEVNCAMASKATTIRMF 180
Db 119 RYFQGLTDPPOESYTTITVLVPPRNIMIDIQKDTAVEGEIEVNCAMASKATTIRMF 178
QY 181 KGNTELKGSKEVEEWSMVTYTSQMLKVKHEDDGVVICQVEHPAVTGNLQTORYLEVQ 240
Db 179 KGNTELKGSKEVEEWSMVTYTSQMLKVKHEDDGVVICQVEHPAVTGNLQTORYLEVQ 238
QY 241 YKQOVHLOMTYPLQGLTREGDALITCEAIGKPOVAVTVWRVDEMPQHAVISGPRLEFI 300
Db 239 YKQOVHLOMTYPLQGLTREGDALITCEAIGKPOVAVTVWRVDEMPQHAVISGPRLEFI 298
QY 301 NNINKTNGTYRCASNIVGKASDYMLYYDPEPTIIPPTTTTTTTTTTTTTTTTTLITD 360
Db 299 NNINKTNGTYRCASNIVGKASDYMLYYDPEPTIIPPTTTTTTTTTTTTTTTTTLITD 358
QY 361 SRAGEBSIRVADAVIGVAVVFMALCLIIILGTVFARHKTYYTHAKADPADADA 440
Db 359 SRAGEBSIRVADAVIGVAVVFMALCLIIILGTVFARHKTYYTHAKADPADADA 418
QY 421 DTALINAGGQNNSEKEKEFYI 442
Db 419 DTALINAGGQNNSEKEKEFYI 440
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RESULT 12

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US-09-944-457-61
: Sequence 61, Application US/09944457
: Patent No. US20020110859A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin
: APPLICANT: Bocstein, David
: APPLICANT: Baton, Dan
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gerritsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Grimaldi, Paul
: APPLICANT: Gurney, Austin
: APPLICANT: Hillan, Kenneth
: APPLICANT: Kljavin, Ivar
: APPLICANT: Napier, Mary
: APPLICANT: Roy, Margaret
: APPLICANT: Tumas, Daniel
: APPLICANT: Wood, William
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P2548P1C1
: CURRENT APPLICATION NUMBER: US/09/944.457
: CURRENT FILING DATE: 2001-09-26
: PRIOR APPLICATION NUMBER: 09/866,028
: PRIOR FILING DATE: 2001-05-25
: PRIOR APPLICATION NUMBER: 60/067,411
: PRIOR FILING DATE: December 3, 1997
: PRIOR APPLICATION NUMBER: 60/069,334
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,335
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,278
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,425
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: PRIOR FILING DATE: December 12, 1997
: PRIOR APPLICATION NUMBER: 60/069,696
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,694
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,702
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,870
: PRIOR FILING DATE: December 17, 1997
: PRIOR APPLICATION NUMBER: 60/069,873
: PRIOR FILING DATE: December 17, 1997
: PRIOR APPLICATION NUMBER: 60/068,017
: PRIOR FILING DATE: December 18, 1997
: PRIOR APPLICATION NUMBER: 60/070,440
: PRIOR FILING DATE: January 5, 1998
: PRIOR APPLICATION NUMBER: 60/074,086
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/074,092
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/075,945
: PRIOR FILING DATE: February 25, 1998
: PRIOR APPLICATION NUMBER: 60/112,850
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 60/113,296
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 60/146,222
: PRIOR FILING DATE: July 28, 1999
: PRIOR APPLICATION NUMBER: PCT/US98/19330
: PRIOR FILING DATE: September 16, 1998
: PRIOR APPLICATION NUMBER: PCT/US98/25108
: PRIOR FILING DATE: December 1, 1998
: PRIOR APPLICATION NUMBER: 09/216,021
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 09/218,517
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 09/254,311
: PRIOR FILING DATE: March 3, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/12252
: PRIOR FILING DATE: June 22, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: September 15, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28409
: PRIOR FILING DATE: No. US20020110859A1ember 30, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28313
: PRIOR FILING DATE: No. US20020110859A1ember 30, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28301
: PRIOR FILING DATE: December 1, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: December 16, 1999
: PRIOR APPLICATION NUMBER: PCT/US00/03565
: PRIOR FILING DATE: February 11, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: February 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/05841
: PRIOR FILING DATE: March 2, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/08439
: PRIOR FILING DATE: March 30, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/14042
: PRIOR FILING DATE: May 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/20710
: PRIOR FILING DATE: July 28, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/32678
: PRIOR FILING DATE: December 1, 2000
: PRIOR APPLICATION NUMBER: PCT/US01/06520
: PRIOR FILING DATE: February 28, 2001
: SEQ ID NO 61
: LENGTH: 440
: TYPE: PRT
: ORGANISM: Homo Sapien
```

US-09-944-457-61
Query Match 99.1%; Score 2263; DB: 9; Length 440;

Best Local Similarity 99.5%; Pred. No. 3.8e-175;
Matches 440; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

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DB 1 MASVYVSGSGCAAAAAAAPPGLRLLLLLPSAALLITGCGNLFYDVTVIGERA 58
QY 61 TISQVVKSDSDSVQLNPNRQTYFPDPRPLKDSRQQLNFSSELKVSILTVS:SDS3 120
DB 59 TISQVVKSDSDSVQLNPNRQTYFPDPRPLKDSRQQLNFSSELKVSILTVS:SDS3 118
QY 121 RYFQOLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEIENVCTAMASKATTIRNF 180
DB 119 RYFQOLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEIENVCTAMASKATTIRNF 178
QY 181 KGNTELKGSKEVEKSMWMTYTSQMLKVKHEDGVVICQVHPATVGLQTORLIEVQ 240
DB 179 KGNTELKGSKEVEKSMWMTYTSQMLKVKHEDGVVICQVHPATVGLQTORLIEVQ 238
QY 241 YKQVPHIQMTYPLQGLTREGDALELTCEAIQKQPVMTVWVAVDDEMPQHAVLSGNLFI 300
DB 239 YKQVPHIQMTYPLQGLTREGDALELTCEAIQKQPVMTVWVAVDDEMPQHAVLSGNLFI 298
QY 301 NNLMKTNGTGRCAASNVGKASHDVMLYYDPTTTPPTTTTTTTTTTTTTTTTT 360
DB 299 NNLMKTNGTGRCAASNVGKASHDVMLYYDPTTTPPTTTTTTTTTTTTTTTTT 358
QY 361 SRAGESSIRAVDAVIGVAVVVFAMLCILLIGYFPAHKQYFTEBANKGADADA 420
DB 359 SRAGESSIRAVDAVIGVAVVVFAMLCILLIGYFPAHKQYFTEBANKGADADA 418
QY 421 DTAINNEGQNNSEKKEYFI 442
DB 419 DTAINNEGQNNSEKKEYFI 440
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RESULT 13

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US-09-944-862-61
; Sequence 61, Application US/09944862
; Patent No. US20020115145A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Baton, Dan
; APPLICANT: Filvarolf, Ellen
; APPLICANT: Gottisen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillar, Kenneth
; APPLICANT: Kijavich, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,862
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
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```
;; PRIOR FILING DATE: December 12, 1997
;; PRIOR APPLICATION NUMBER: 60/069,696
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,694
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,702
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,870
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/069,873
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/068,017
;; PRIOR FILING DATE: December 18, 1997
;; PRIOR APPLICATION NUMBER: 60/070,440
;; PRIOR FILING DATE: January 5, 1998
;; PRIOR APPLICATION NUMBER: 60/074,086
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/074,092
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/075,945
;; PRIOR FILING DATE: February 25, 1998
;; PRIOR APPLICATION NUMBER: 60/112,850
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 60/113,236
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 60/146,222
;; PRIOR FILING DATE: July 28, 1999
;; PRIOR APPLICATION NUMBER: PCT/US98/19330
;; PRIOR FILING DATE: September 16, 1998
;; PRIOR APPLICATION NUMBER: PCT/US98/25108
;; PRIOR FILING DATE: December 1, 1998
;; PRIOR APPLICATION NUMBER: 09/216,021
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 09/218,517
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 09/254,311
;; PRIOR FILING DATE: March 3, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: June 22, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: September 15, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28409
;; PRIOR FILING DATE: No. US20020115145A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: No. US20020115145A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28301
;; PRIOR FILING DATE: December 1, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: December 16, 1999
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: February 28, 2001
;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO: 61
;; LENGTH: 440
;; TYPE: PRT
;; ORGANISM: Homo Sapien
```

Query Match 99.1%; Score 2263; DB 9; Length 440;

Best Local Similarity 99.5%; Pred. No. 3,8e-175;
Matches 440; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

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OY 1 MASVTLPSGSCCAAAAAAAPPGLRLRLILLLFSAALIPGDCQNTFKDVVIEGEVA 60
DB 1 MASVTLPSGSCCAAAAAAAPPGL--LRLLILLLFSAALIPGDCQNTFKDVVIEGEVA 58
OY TISCVNKSDDSVQLNPNRQTYFRDPRFLKDSRQQLNFSSELKXSLTNVSIISDEG 120
DB TISCVNKSDDSVQLNPNRQTYFRDPRFLKDSRQQLNFSSELKXSLTNVSIISDEG 118
OY TISCVNKSDDSVQLNPNRQTYFRDPRFLKDSRQQLNFSSELKXSLTNVSIISDEG 118
DB TISCVNKSDDSVQLNPNRQTYFRDPRFLKDSRQQLNFSSELKXSLTNVSIISDEG 118
OY RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKTAVERIEVNCJAMASKPATIIRWF 180
DB RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKTAVERIEVNCJAMASKPATIIRWF 178
OY KGNTEIKGKSEVEEMSDMYTTSQMLKVKHEDGVPICQVEHPATVGNLQTRYLEVQ 240
DB KGNTEIKGKSEVEEMSDMYTTSQMLKVKHEDGVPICQVEHPATVGNLQTRYLEVQ 238
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DB YKPOVHLQMTYPLQGLTREGDALELTCEALGKPOVWVTVWRVDENPOHAYLSGPLYFI 298
OY NNKKTNDNGTYRCASNVGKASHDYMLYTDPPTTTPPTTTTTTTTTTTTTTTTTTTTT 360
DB NNKKTNDNGTYRCASNVGKASHDYMLYTDPPTTTPPTTTTTTTTTTTTTTTTTTTTT 358
OY SRAGEGSIKRAVDNAVIGVAVVFMALCLLILGTFARHKGYTFTHAKGADDAADA 420
DB SRAGEGSIKRAVDNAVIGVAVVFMALCLLILGTFARHKGYTFTHAKGADDAADA 418
OY DTALINAEQGQNNSEKKEFYI 442
DB DTALINAEQGQNNSEKKEFYI 440

RESULT 14
US-09-945-587-61
; Sequence 61, Application US/09945587
; Patent No. US20020127643A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gunney, Austin
; APPLICANT: Hillman, Kenneth
; APPLICANT: Kijavich, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/945,587
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
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; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
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; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 23, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020127643A1, September 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020127643A1, September 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-945-587-61
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Query Match 99.1%; Score 2263; DB 9; Length 440;

Best Local Similarity 99.5%; Pred. No. 3.8e-175;
Matches 440; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

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Cy 241 YKPOVHIQMTYPLQGLTRREGDALELTCFAIGKQPPVMTWVRVDEMPQHAVISGNLFI 300
Db 239 YKPOVHIQMTYPLQGLTRREGDALELTCFAIGKQPPVMTWVRVDEMPQHAVISGNLFI 298
Cy 301 NNLNKTNGTTRGCAASNIYVKAHSDYMLYYDDPTTIPPTTTTTTTTTTTTTTTTT 360
Db 299 NNLNKTNGTTRGCAASNIYVKAHSDYMLYYDDPTTIPPTTTTTTTTTTTTTTTTT 358
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RESULT 15
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Sequence 61, Application US/09945015
Patent No. US20020132768A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Batstein, David
APPLICANT: Bacon, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gettitsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavlin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/945,015
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
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PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425

PRIOR FILING DATE: December 12, 1997
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PRIOR APPLICATION NUMBER: 60/069,694
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PRIOR FILING DATE: December 17, 1997
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PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
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PRIOR APPLICATION NUMBER: 60/146,222
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PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
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PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020132768A1, December 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020132768A1, December 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
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PRIOR FILING DATE: May 22, 2000
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PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LENGTH: 440
TYPE: PRT
ORGANISM: Homo Sapien
US-09-945-015-61

Query Match 99.1%; Score 2263; DB 9; Length 440;

Best Local Similarity 99.5%; Pred. No. 3.8e-175;
Matches 440; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

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Qy	361	SRAGEEGSIRAVDAVIGVVAVVFAMLCLLILGRYFARHKGTFTHEAKGADADA	420
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CM protein - protein search, using sw model

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Title: US-10-622-237-2

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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database : Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2283	100.0	442	4 US-09-930-803-1	Sequence 1, Appl
3	2263	99.1	440	4 US-09-866-028-61	Sequence 61, Appl
4	2169	95.0	423	4 US-09-778-510-22	Sequence 22, Appl
5	902	39.5	444	2 US-08-659-984A-5	Sequence 5, Appl
6	902	39.5	444	2 US-08-660-531-5	Sequence 5, Appl
7	895.5	39.2	421	2 US-08-659-984A-1	Sequence 1, Appl
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10	739	32.4	398	4 US-09-778-510-6	Sequence 6, Appl
11	739	32.4	398	4 US-09-907-794A-84	Sequence 84, Appl
12	739	32.4	398	4 US-09-905-125A-84	Sequence 84, Appl
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14	722	31.6	432	4 US-09-778-510-2	Sequence 2, Appl
15	335	11.2	517	4 US-09-205-258-947	Sequence 947, App
16	256.5	11.7	518	4 US-09-723-368-4	Sequence 4, Appl
17	248	10.9	518	4 US-09-919-172-20	Sequence 20, Appl
18	232	10.2	393	4 US-08-429-742-2	Sequence 2, Appl
19	226	9.9	479	4 US-09-723-368-2	Sequence 2, Appl
20	222	9.7	458	4 US-09-435-956A-1	Sequence 1, Appl
21	220.5	9.7	344	4 US-09-700-397-3	Sequence 3, Appl
22	211	9.2	313	4 US-09-700-397-4	Sequence 4, Appl
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26	206	9.0	734	2 US-08-389-459A-17	Sequence 17, Appl
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44	198.5	8.7	408	4 US-09-724-864-62	Sequence 62, Appl
45	197.5	8.7	338	2 US-08-414-657D-60	Sequence 60, Appl

ALIGNMENTS

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US-09-778-510-20					
Sequence 20, Application US/09778510					
Patent No. 6512095					
GENERAL INFORMATION:					
APPLICANT: Baum, Peter					
TITLE OF INVENTION: Molecules Designated B7L1					
FILE REFERENCE: 2844-US					
CURRENT APPLICATION NUMBER: US/09/778,510					
CURRENT FILING DATE: 2001-02-07					
PRIOR APPLICATION NUMBER: PCT/US99/17906					
PRIOR FILING DATE: 1999-08-05					
PRIOR APPLICATION NUMBER: 60/095,663					
PRIOR FILING DATE: 1998-08-07					
NUMBER OF SEQ ID NOS: 22					
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SEQ ID NO 20					
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TYPE: PRT					
ORGANISM: Homo sapien					
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QY	61	TISCCVKNKDDSVI	QLNPNRQTIYFRDPR	LKXDRFQNLN	SSSELKXSLNVSISD
DB	61	TISCCVKNKDDSVI	QLNPNRQTIYFRDPR	LKXDRFQNLN	SSSELKXSLNVSISD
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DB	121	RFFCQLYTDP	PEESYTTITVLV	PPNNLMID	IKDTAVGEEIEVNC
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QY 361 SRAGEGSIKAVDAHVIGVAVVVFAMCLLIIIGRYFARHKGTYFTHAKGADDAADA 420
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QY 421 DTAINAEGGONNSEKKEYFI 442
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RESULT 2

US-09-930-803-1
; Sequence 1, Application US/09930803
; Patent No. 6596493
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: REEVES, Roger
; APPLICANT: YOSHINO, Mamiaki
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS
; FILE REFERENCE: JUL1770-1
; CURRENT APPLICATION NUMBER: US/09/930,803
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-930-803-1

Query Match 100.0%; Score 2283; DB 4; Length 442;
Best Local Similarity 100.0%; Pred. No. 6,6e-192;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 421 DTAINAEGGONNSEKKEYFI 442
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RESULT 3

US-09-866-028-61
; Sequence 61, Application US/09866028
; Patent No. 6642360
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David

APPLICANT: Baton, Dan
APPLICANT: Perrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gettleson, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavich, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2148P1C1
CURRENT APPLICATION NUMBER: US/09/866,028
CURRENT FILING DATE: 2001-05-25
Prior application data removed - consult PAM or file wrapper
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LENGTH: 440
TYPE: PRT
ORGANISM: Homo Sapien
US-09-866-028-61

Query Match 99.1%; Score 2263; DB 4; Length 440;
Best Local Similarity 99.5%; Pred. No. 3,7e-190;
Matches 440; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 MASVLPESGSCAAAAAAPPGLRLRLIIIFSAALIPFGDONLFTKDVYVIEBEVA 60
Db 1 MASVLPESGSCAAAAAAPPGLRLRLIIIFSAALIPFGDONLFTKDVYVIEBEVA 58
QY 61 TISCOVNSDSDSVIQLNPNKQTIYFRDFRPLKDSRFQLNFSSELKVSITNVSISDEG 120
Db 59 TISCOVNSDSDSVIQLNPNKQTIYFRDFRPLKDSRFQLNFSSELKVSITNVSISDEG 118
QY 121 RYFCQLYTDPQESYTTITVLPVPRNLMIDIQKOTAVEGEEIENVCTAMASKPATITRMF 180
Db 119 RYFCQLYTDPQESYTTITVLPVPRNLMIDIQKOTAVEGEEIENVCTAMASKPATITRMF 178
QY 181 KNTTELKGSSEVEEWSMDVYVTSQMLKVHKEDDGVPIICQVEHPAVTGNLQOTORYLEVQ 240
Db 179 KNTTELKGSSEVEEWSMDVYVTSQMLKVHKEDDGVPIICQVEHPAVTGNLQOTORYLEVQ 238
QY 241 YKPOVHIQMTYPLQGLTRREGDALBELTCEAIGKQPQVMTWVRVDDEMPQHAVALSGPNLFI 300
Db 239 YKPOVHIQMTYPLQGLTRREGDALBELTCEAIGKQPQVMTWVRVDDEMPQHAVALSGPNLFI 298
QY 301 NNUNKTNDGTGRCEASNIVGKASHDYMUYVDPPTTIPPTTTTTTTTTTTTTTTTTTTTT 360
Db 299 NNUNKTNDGTGRCEASNIVGKASHDYMUYVDPPTTIPPTTTTTTTTTTTTTTTTTTTTT 358
QY 361 SRAGEGSIKAVDAHVIGVAVVVFAMCLLIIIGRYFARHKGTYFTHAKGADDAADA 420
Db 359 SRAGEGSIKAVDAHVIGVAVVVFAMCLLIIIGRYFARHKGTYFTHAKGADDAADA 418
QY 421 DTAINAEGGONNSEKKEYFI 442
Db 419 DTAINAEGGONNSEKKEYFI 440

RESULT 4

US-09-778-510-22
; Sequence 22, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510

CURRENT FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: PCT/US99/17906
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: 60/095,663
NUMBER OF SEQ ID NOS: 1996-08-07
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 22
LENGTH: 423
TYPE: PRT
ORGANISM: Mus musculus
US-09-778-510-22

Query Match 95.0%; Score 2169; DB 4; Length 423;
Best Local Similarity 98.8%; Pred. No. 6,1e-182;
Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 19 AAPPGLRLRLLLFFSAAALPTGDDGQLFTKDVTEGEVATISCCVNSDDSVIQLLN 78
DB 1 AAPPGLRLRLLLSSAALPTGDDGQLFTKDVTEGEVATISCCVNSDDSVIQLLN 60
QY 79 PNRQTIYFRDPRPKDSRFQLLNFSSELKVLTVNSISDEGRYFCQLYTDPQESYTTI 138
DB 61 PNRQTIYFRDPRPKDSRFQLLNFSSELKVLTVNSISDEGRYFCQLYTDPQESYTTI 120
QY 139 TVLVPRLMTDQKQRAVEGEELVNCTAMASRPATTIRFKKNTLKGSEVEEWSDM 198
DB 121 TVLVPRLMTDQKQRAVEGEELVNCTAMASRPATTIRFKKNTLKGSEVEEWSDM 180
QY 199 YTVTSQMLKVKHKEDDGVFVLCQVEHPAVTGNLTQRYLEVOYKPOVHIMTYPLQGLTR 258
DB 181 YTVTSQMLKVKHKEDDGVFVLCQVEHPAVTGNLTQRYLEVOYKPOVHIMTYPLQGLTR 240
QY 259 EGDALETCEAIGRPQVMTWVAVDDMPQHAVLSGPNLPINNLTNDNGTYRCEASNT 318
DB 241 EGDALETCEAIGRPQVMTWVAVDDMPQHAVLSGPNLPINNLTNDNGTYRCEASNT 300
QY 319 VGKASDYMXYVDPPTTTPPTTTTTTTTTTTTTTTTTTDSAGEEGSIRAVDAVIG 378
DB 301 VGKASDYMXYVDPPTTTPPTTTTTTTTTTTTTTTTTTDSAGEEGSIRAVDAVIG 360
QY 379 GVAVAVVFPAMCLIIIGRYFARHKGYFTHEAKGADDAADATAIINAEQGNSEKK 438
DB 361 GVAVAVVFPAMCLIIIGRYFARHKGYFTHEAKGADDAADATAIINAEQGNSEKK 420
QY 439 EYF 441
DB 421 EYF 423

RESULT 5
US-08-659-984A-5
Sequence 5, Application US/08659984A
Patent No. 5943400
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Sinha, Sukanto
APPLICANT: Jacobson-Croak, Kirsten L.
TITLE OF INVENTION: Assays for Detecting Beta-Secretase
TITLE OF INVENTION: Inhibition
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,984A
FILING DATE: 07-JUN-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002810US
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-659-984A-5

Query Match 39.5%; Score 902; DB 2; Length 444;
Best Local Similarity 44.6%; Pred. No. 8.3e-71;
Matches 194; Conservative 74; Mismatches 137; Indels 30; Gaps 7;

QY 31 LIFSAAA---LPTDGGQLFTKDVTEGEVATISCCVNSDDSVIQLNRRQTIYFR 87
DB 17 LIFSAAA---LPTDGGQLFTKDVTEGEVATISCCVNSDDSVIQLNRRQTIYFR 76
QY 88 DFRPKDSRFQLLNFSSELKVLTVNSISDEGRYFCQLYTDPQESYTTITVLVPPRL 147
DB 77 DFRPKDSRFQLLNFSSELKVLTVNSISDEGRYFCQLYTDPQESYTTITVLVPPRL 136
QY 148 MIDQKQRAVEGEELVNCTAMASRPATTIRFKKNTLKGSEVEEWS---DMYTVSQ 204
DB 137 MIDQKQRAVEGEELVNCTAMASRPATTIRFKKNTLKGSEVEEWS---DMYTVSQ 196
QY 205 LMLKVKHKEDDGVFVLCQVEHPAVTGNLTQRYLEVOYKPOVHIMTYPLQGLTR 263
DB 197 LMLKVKHKEDDGVFVLCQVEHPAVTGNLTQRYLEVOYKPOVHIMTYPLQGLTR 253
QY 264 ELTCAIGRPQVMTWVAVDDMPQHAVLSGPNLPINNLTNDNGTYRCEASNT 321
DB 254 ELTCAIGRPQVMTWVAVDDMPQHAVLSGPNLPINNLTNDNGTYRCEASNT 313
QY 322 AHSDFYLVYVDPPTTTPPTTTTTTTTTTTTTTTTTTDSAGEEGSIRAVDAVIG 367
DB 314 AHSDFYLVYVDPPTTTPPTTTTTTTTTTTTTTTTTTDSAGEEGSIRAVDAVIG 373
QY 368 SIRAVDAVIGVAVVFPAMCLIIIGRYFARHKGYFTHEAKGADDAADATAIINA 427
DB 374 SIRAVDAVIGVAVVFPAMCLIIIGRYFARHKGYFTHEAKGADDAADATAIINA 429
QY 428 EGGVNSSEKKYF 442
DB 430 EGGVNSSEKKYF 444

RESULT 6
US-08-660-531-5
Sequence 5, Application US/08660531
Patent No. 6221645
GENERAL INFORMATION:
APPLICANT: Chrysler, Susanna M.S.
APPLICANT: Sinha, Sukanto
APPLICANT: Keim, Pamela S.
APPLICANT: Anderson, John P.
TITLE OF INVENTION: Beta-Secretase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,531
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,498
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002210US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-660-531-5

Query Match 39.5%; Score 902; DB 3; Length 444;
Best Local Similarity 44.6%; Pred. No. 8,38-71;
Matches 194; Conservative 74; Mismatches 137; Indels 30; Gaps 7;

31 LLEFSA--LIFGCGNLFYKYVYIEGEVATISQVYKSDSVYQLNPNRQTIYR 87
17 LLLQAAAKNKVKSGGQFPLTQNTVVEGFTALITCRVDNDNTSLQWNPAAQOTLYFD 76
88 DFRPKDSRFLQNLNFSSELKVLSTNVISDEGRYFCQLYTDPQESYTTITVLPNNIL 147
77 DKKALRDRRIELVRSWHELSISVSDLSDEGQYCSLTTPVKSKALTYLVGPEKP 136
148 MIDQKDTAVGEELIYVNCYTNASKPATITRMFKGNTLKGKSEVEEWS---DMYTVTSQ 204
137 QISGSSSVMEGDLMLQTLCKTSGSKSPADIRMFNDKEIKDVYKKEEDANRKTFTVSSST 196
205 LMLKYHKEDDGVPIYQVEHPAVTGNLQ--TQRYLVEVYKPOVHIQMTYPLQGLTREGDAL 263
197 LDFRDRSDGVAVICRVHESLNATQVAMQVLEIHTSVKI---IPSTFPQEGPL 253
264 ELTCATGKPOPVNTYKRVDDEN--POHAYLSEPNLFINLNKTDNGTYRCASNTVKG 321
254 ILTCSGSKPLPEPLMTKDGELPDPDRVVSRELNILFNKTDNGTYRCATYTIQ 313
322 AHSDFMLVYDPTTIPPTTT 367
314 SSAEVLIVHVPNTLPTTIIIPSLTATVTTVAITTSPTTSATSSIRDPNALAGQNG 373
368 SIRAVDAVIGVAVVVFAMLCILILIGRYPARHKTGTYTHKAGDADADATAIINA 427
374 P---DHALIGGIYAVVVFVTLCSIFLIGRYLAHKGYLVINAKAGADAPDADTAIINA 429
428 EGGQNNSEKKEFYI 442
430 EGGQVNAEKEKEFYI 444

RESULT 7
US-08-659-984A-1
; Sequence 1, Application US/08659984A

Patent No. 5942400
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Sinha, Sukanto
APPLICANT: Jacobson-Croak, Kirsten L.
TITLE OF INVENTION: Assays for Detecting Beta-Secretase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,984A
FILING DATE: 07-JUN-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002810US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-659-984A-1

Query Match 39.2%; Score 895.5; DB 2; Length 421;
Best Local Similarity 45.1%; Pred. No. 2,9e-70;
Matches 189; Conservative 73; Mismatches 130; Indels 27; Gaps 6;

44 GONLFTQVYIEGEVATISQVYKSDSVYQLNPNRQTIYFRPKDSRFLQNLNFS 103
10 GQPLTQNTVVEGFTALITCRVDNDNTSLQWNPAAQOTLYFDKKALRDRRIELVRS 69
104 SSELKVLSTNVISDEGRYFCQLYTDPQESYTTITVLPNNIMIDQKDTAVGEELI 163
70 WHELSISVSDLSDEGQYCSLTTPVKSKALTYLVGPEKPOLISGSSSVMEGDLMLQ 129
164 VNCTANASKPATITRMFKGNTLKGKSEVEEWS---DMYTVTSQMLKYHKEDDGVPIY 220
130 LTKTSGSKPADIRMFNDKEIKDVYKKEEDANRKTFTVSSSTLDFRDRSDGVAVIC 189
221 QVEHPATVGNLQ--TQRYLVEVYKPOVHIQMTYPLQGLTREGDALETCAIGKPOPVNT 279
190 RVHESLNATQVAMQVLEIHTSVKI---IPSTFPQEGPLILTCSGSKPLPEPL 246
280 WVRVDDEN--POHAYLSEPNLFINLNKTDNGTYRCASNTVKGASDYMALVYDPTT 337
247 WTKGQGLPDPDRVVSRELNILFNKTDNGTYRCATNTIGQSSAEVLLIVHVPNTL 306
338 PPTTT 383
307 LPTIIIPSLTATVTTVAITTSPTTSATSSIRDPNALAGQNG---DHALIGGIYAV 362
384 VFAMLCILILIGRYPARHKTGTYTHKAGDADADATAIINAEGQNNSEKKEFYI 442

Db 363 VVFVTLCSIFILGRYLARHKGTLYLTNKAKEADAPDADTALINAEQQVNAEKEKEYFI 421

RESULT 8

US-08-660-531-1
Sequence 1, Application US/08660531
Patent No. 6221645
GENERAL INFORMATION:
APPLICANT: Chrysler, Susanna M.S.
APPLICANT: Simha, Sukanto
APPLICANT: Keim, Pamela S.
APPLICANT: Anderson, John P.
TITLE OF INVENTION: Beta-Secretase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,531
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,498
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002210US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-660-531-1

Query Match 39.2%; Score 895.5; DB 3; Length 421;
Best Local Similarity 45.1%; Pred. No. 2,9e-70;
Matches 189; Conservative 73; Mismatches 130; Indels 27; Gaps 6;

QY 44 GQNLFFKQVTVIEGEVATISQVYKSDSVIQLNPNRQTYFFDFPLKNSRQLNFS 103
DB 10 GGFPLQONTVVEGGTALITCRVDNDNTSLQMSNPAQOYTFPDKALRNRLTELVRAS 69
QY 104 SSELKVLTVNVSISDEGRYFCQLYTDPQESYTTITVLPNNIMIDIQKTAVEGEIE 163
DB 70 WHLELSVSDVLSDBGQYTCGLTFMPVKTSKAYITVIGVEKQDISFSSFWNEGDMQ 129
QY 164 VNCTAMASRPATTTIRKENTELKGSVEEVS--DWTYTSQMLKVKHKEDGVPYIC 220
DB 130 LTCTKTSGRPADIRFKNKDKIKQVKYLRKEDANRKTFTVSTLDFVRDSDGVAVIC 189
QY 221 QVEHPAVTGNLQ--TORYLEVOYKPOVHIQMTYPLQGLTREGDALELTCEAIKQPVMVT 279
DB 190 RVDHESLNTPCVAMQVLEIHTPSVKI--IPSTPFGQEPILITCESKGRPLPEVYL 246
QY 280 WRAVDDEM--POHAYISGNPLFINLNKTDNGTYRCEASNVGKAHSHYMLVYDPTTI 337
DB 247 WTKDGGELPDPKRMVSVGRLELILPLNKTDNGTYRCEATNTIGSSAEYVILVHDVNTL 306

QY 338 PPTTTTNTTTTNTTTTNTTTT-----DSRAGEBSIRADVAVIGGVAV 383
DB 307 LPTTIPSLTAVTAVTTTVAITTSPTTSATTSIRDPNALAGQNP-----DHALIGIVAV 362
QY 384 VFMALCLLITLGRYFPRKHGTFTHEAKGADPADADTALINAEQQVNAEKEKEYFI 442
DB 363 VVFVTLCSIFILGRYLARHKGTLYLTNKAKEADAPDADTALINAEQQVNAEKEKEYFI 421

RESULT 9

US-09-778-510-4
Sequence 4, Application US/09778510
Patent No. 6512095
GENERAL INFORMATION:
APPLICANT: Baum, Peter
TITLE OF INVENTION: Molecules Designated B7L1
FILE REFERENCE: 2844-US
CURRENT FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: PCT/US99/17906
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: 60/035,663
PRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 398
TYPE: PRT
ORGANISM: Mus musculus
US-09-778-510-4

Query Match 32.7%; Score 745.5; DB 4; Length 398;
Best Local Similarity 39.1%; Pred. No. 3,7e-57;
Matches 172; Conservative 74; Mismatches 137; Indels 57; Gaps 11;

QY 16 AAAAPPGRLRLILLLESAAALIPG-----DQNLFTQDVYIEGEVATISQVYKSD 70
DB 3 APAASP-----VPLILL--ACSNAPGANLSQDSQWTSDETVAGTVLCKQVADHE 56
QY 71 DSVIQLNPNRQTYFFDFPLKNSRQLNFSSELKVLTVNISISDEGRYFCQLYTDP 130
DB 57 DSSLQMSNPAQOYTFCEKRALRNRIQLVSTFHELSISISVALADEEYTCSTPTMP 116
QY 131 PQESYTTITVLPNNIMIDIQKTAVEGEIEVNCTAMASKPATTTIRKGNTELKG-K 189
DB 117 VATAKSLVTVLGIPOKPIITGYKSLREKETATLNCSSGSKRPAQLTWKQDELHGDQ 176
QY 190 SEVEEMSD--MYTTSQMLKVKHKEDGVPYICQVEHPAVTG-NLQTORYLEVOYKPOVH 246
DB 177 TRIQEDPNKTFVSSSVSFQVTRDDGANIVCSVNHESLKGADRSTSORIEVLYTPTAM 236
QY 247 IQMTYPLQGLTREGDALELTCEAIKGPVVMVTWRAVDDEM--QHAVISGNPLINN 302
DB 237 IR--PEPAHPRREGKLLHCEGKNVPQQYVWVKGSSEPLKMTGESALIF-----F 268
QY 303 LNKTDNGTYRCEASNVGKAHSDYMLVYDPTTIPTTTTNTTTTNTTTTILITIDSR 362
DB 289 LNKSDSGTYGCATSNMGSYTAFTLVNDPS---PVPSSSTY----- 329
QY 363 AEEBSIRAVDPNAVIGVAVVFMALCLLITLGRYFPRKHGTFTHEAKGADPADADT 422
DB 330 -----HAIGGIYAVIFELILILFLGHYILRHKGTYLTHEAKGSDPADADT 378
QY 423 AINAEQQVNAEKEKEYFI 442
DB 379 AINAEQQVNAEKEKEYFI 398

RESULT 10

US-09-778-510-6
Sequence 6, Application US/09778510
Patent No. 6512095
GENERAL INFORMATION:

```

/ APPLICANT: Baum, Peter
/ TITLE OF INVENTION: Molecules Designated B7L1
/ FILE REFERENCE: 2844-US
/ CURRENT APPLICATION NUMBER: US/09/778,510
/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: PCT/US99/17906
/ PRIOR FILING DATE: 1999-08-05
/ PRIOR APPLICATION NUMBER: 60/095,663
/ PRIOR FILING DATE: 1998-08-07
/ NUMBER OF SEQ ID NOS: 22
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 6
/ LENGTH: 398
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-778-510-6

Query Match          32.4%; Score 739; DB 4; Length 398;
Best Local Similarity 38.6%; Pred. No. 1,4e-56;
Matches 166; Conservative 73; Mismatches 147; Indels 44; Gaps 9;

QY 22 PGLRLRLILFLSAAALIPG-----DQNLFTKDVYIEGEVATISQVKNKSDSVYQL 76
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 4 PAASLLILLLLF-ACMAAPGAGNLSDDSQPMTSDETVAGTVVLCQVQDHDHDSLOW 62

QY 77 LNPNRQTIYFRDPRPLKDSRFOLNFSSELKVLTVNVSIDEGRYFCOLYTPPOESYT 136
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 63 SNPAQGTLYFGKRALRDRNRQIVTSTPHLSISINVALADEGEYTCISIFMPVPTAKS 122

QY 137 TITVYVPPRLMIDIQKTAIVEGEIEVNCIAMSKEPATITIRWKGTELKXK-SEVEEM 195
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 123 LVTVLGIPOKPIITGYKSSIREKDTATLNCSSGSKPAARLTWRKGDQELHGEPTRIOED 182

QY 196 SD--MYVTISQMLKXHKHEDDGVFVICOVEHPAVTG-NLQTORLLEYQYKQVHIQWTP 252
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 189 PDKFTYVSSVTFQVTRHEDDASIVCSVNHESLKGADRSTQRIEVLTPYTMIRDPDP 242

QY 253 LOGLRREGDALELTGAIGKQOPVWTVWRVDDMPQANVLSGNLFINNLANTDNGTTR 312
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 243 --HPRREGQKLLHREGGNVPOQYIWEK-EGSVPLPKQTOESALFPPLNKSDSGTYG 298

QY 313 CEASNIYVKASDYLIVYDPPFTLIPPTTTTTTTTTTTTTTTTTTTTTTTTTTIDSPAGEGSI 372
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 299 CNAISNMSYKAYVILNNDPS---PVSSSSSTY----- 329

QY 373 DNAYVGVVAVVYFMLELLIILIGRYFARKGTYFTHEANGADADADADATAIINAGGON 432
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 330 -HAITGGIVAFIVFLILMLIFLGHYILRHKGTYLTHEANGSDADPADTAIINAGGOS 388

QY 433 NSEKKKEYFI 442
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 389 GGDDKKKEYFI 398

RESULT 11
US-09-907-794A-84
/ Sequence 84, Application US/09907794A
/ Patent No. 6635468
/ GENERAL INFORMATION:
/ APPLICANT: Genentech, Inc.
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fond, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gettleisen, Mary E.
/ APPLICANT: Goddard, A.
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, Christopher J.

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/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth, J.
/ APPLICANT: Kijavlin, Ivar J.
/ APPLICANT: Mather, Jennie P.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William, I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: 10466-14
/ CURRENT APPLICATION NUMBER: US/09/794A
/ PRIOR FILING DATE: 2001-07-17
/ PRIOR APPLICATION NUMBER: PCT/US00/04414
/ PRIOR FILING DATE: 2000-02-22
/ PRIOR APPLICATION NUMBER: US 60/143,048
/ PRIOR FILING DATE: 1999-07-07
/ PRIOR APPLICATION NUMBER: US 60/145,698
/ PRIOR FILING DATE: 1999-07-26
/ PRIOR APPLICATION NUMBER: US 60/146,222
/ PRIOR FILING DATE: 1999-07-28
/ PRIOR APPLICATION NUMBER: PCT/US99/20594
/ PRIOR FILING DATE: 1999-09-08
/ PRIOR APPLICATION NUMBER: PCT/US99/20944
/ PRIOR FILING DATE: 1999-09-13
/ PRIOR APPLICATION NUMBER: PCT/US99/21090
/ PRIOR FILING DATE: 1999-09-15
/ PRIOR APPLICATION NUMBER: PCT/US99/21547
/ PRIOR FILING DATE: 1999-09-15
/ PRIOR APPLICATION NUMBER: PCT/US99/23089
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: PCT/US99/28214
/ PRIOR FILING DATE: 1999-11-29
/ PRIOR APPLICATION NUMBER: PCT/US99/28313
/ PRIOR FILING DATE: 1999-11-30
/ PRIOR APPLICATION NUMBER: PCT/US99/28564
/ PRIOR FILING DATE: 1999-12-02
/ PRIOR APPLICATION NUMBER: PCT/US99/28565
/ PRIOR FILING DATE: 1999-12-02
/ PRIOR APPLICATION NUMBER: PCT/US99/30095
/ PRIOR FILING DATE: 1999-12-16
/ PRIOR APPLICATION NUMBER: PCT/US99/30911
/ PRIOR FILING DATE: 1999-12-20
/ PRIOR APPLICATION NUMBER: PCT/US99/30999
/ PRIOR FILING DATE: 1999-12-20
/ PRIOR APPLICATION NUMBER: PCT/US00/00219
/ NUMBER OF SEQ ID NOS: 423
/ SEQ ID NO 84
/ LENGTH: 398
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-907-794A-84

Query Match          32.4%; Score 739; DB 4; Length 398;
Best Local Similarity 38.6%; Pred. No. 1,4e-56;
Matches 166; Conservative 73; Mismatches 147; Indels 44; Gaps 9;

QY 22 PGLRLRLILFLSAAALIPG-----DQNLFTKDVYIEGEVATISQVKNKSDSVYQL 76
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DB 4 PAASLLILLLLF-ACMAAPGAGNLSDDSQPMTSDETVAGTVVLCQVQDHDHDSLOW 62

QY 77 LNPNRQTIYFRDPRPLKDSRFOLNFSSELKVLTVNVSIDEGRYFCOLYTPPOESYT 136
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 63 SNPAQGTLYFGKRALRDRNRQIVTSTPHLSISINVALADEGEYTCISIFMPVPTAKS 122

QY 137 TITVYVPPRLMIDIQKTAIVEGEIEVNCIAMSKEPATITIRWKGTELKXK-SEVEEM 195
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 123 LVTVLGIPOKPIITGYKSSIREKDTATLNCSSGSKPAARLTWRKGDQELHGEPTRIOED 182

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QY 196 SD--MYTTSQMLKVKHEDDGVPIQVHEPAVVG-NLQTORYLEVOYKQVHIQMTYP 252
Db 183 PDKGFTYSSVTFOVTRHDDGASIVCSVNHESLGADRSTSORLEVLYTPAMIRPPP 242
QY 253 LOGTREGDALELTCEALIGKQPQVWVTVRVVDEKPEQAVLSGPNLFTNNKNDNGTYR 312
Db 243 ---HREBQKLLHCEGRGNFVPOQYLWEK-EGSVPLKMTQESALIFPFLNKSDSGTYG 298
QY 313 CEASNIVKASHSDVWLVYVDEPTTIPPTTTTTTTTTTTTTTTTTTTTTTDSRAGEGSIKAV 372
Db 229 CTATSNMGSYKAYVTLNVNDS--PVPSSSTY----- 325
QY 373 DHAVIGVAVVAVFAMLLIILIGYFARHKGTYTHAKGADDAADTAIINAEGGON 432
Db 330 -HAIGGIIVAFVFLIIMLIFLGHYLLRHKGTYLTHAKGSDADPADTAIINAEGGOS 388
QY 433 NSEKKEEYFI 442
Db 389 GDDDKKEEYFI 398

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RESULT 12
US-09-905-125A-84

; Sequence 84, Application US/09905125A

; Patent No. 6664376

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: Kijavhin, Ivar J.

; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/905,125A

; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26

; PRIOR APPLICATION NUMBER: US 60/146,222

; PRIOR FILING DATE: 1999-07-28

; PRIOR APPLICATION NUMBER: PCT/US99/20594

; PRIOR FILING DATE: 1999-09-08

; PRIOR APPLICATION NUMBER: PCT/US99/20944

; PRIOR FILING DATE: 1999-09-13

; PRIOR APPLICATION NUMBER: PCT/US99/21090

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/21547

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/23089

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; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 84
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-125A-84

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Query Match 32.4%; Score 739; DB 4; Length 398;
Best Local Similarity 38.6%; Pred. No. 1.4e-56;
Matches 166; Conservative 73; Mismatches 147; Indels 44; Gaps 9;

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QY 22 PGLRLRLLLLSAALITPTG-----DGNLFYKYVTVYEGVATISCVKNSDQSVIQL 76
Db 4 PAASLLLLLLF-ACCMAGGANLSQDQSQPTSDSEYVAGGVVILKQVKNHEDSSIQW 62
QY 77 LNPNRQTYRDPRLPKDSRFQNLNFSSELKVSITNWSISDEGRYFCOLYTPDQESYT 136
Db 63 SNPAQOTLVFGKRALRDRIQVSTHRELSTISNVALDEGYSIFMPRTAKS 122
QY 137 TITVAVPNNMIDIQKOTAVEGEIEVNCNAMASKPATTTTWFKNTLKK-SEVEW 195
Db 123 LVTVIGIPKPLITTYKSKSLREKDTATLNCSSGSKPARILTWKGDQDELHGEPTRID 182
QY 196 SD--MYTTSQMLKVKHEDDGVPIQVHEPAVVG-NLQTORYLEVOYKQVHIQMTYP 252
Db 183 PDKGFTYSSVTFOVTRHDDGASIVCSVNHESLGADRSTSORLEVLYTPAMIRPPP 242
QY 253 LOGTREGDALELTCEALIGKQPQVWVTVRVVDEKPEQAVLSGPNLFTNNKNDNGTYR 312
Db 243 ---HREBQKLLHCEGRGNFVPOQYLWEK-EGSVPLKMTQESALIFPFLNKSDSGTYG 298
QY 313 CEASNIVKASHSDVWLVYVDEPTTIPPTTTTTTTTTTTTTTTTTTTTTTDSRAGEGSIKAV 372
Db 229 CTATSNMGSYKAYVTLNVNDS--PVPSSSTY----- 325
QY 373 DHAVIGVAVVAVFAMLLIILIGYFARHKGTYTHAKGADDAADTAIINAEGGON 432
Db 330 -HAIGGIIVAFVFLIIMLIFLGHYLLRHKGTYLTHAKGSDADPADTAIINAEGGOS 388
QY 433 NSEKKEEYFI 442
Db 389 GDDDKKEEYFI 398

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RESULT 13

US-09-902-775A-84

; Sequence 84, Application US/09902775A

; Patent No. 6686451

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

```

APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Thomas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 84
LENGTH: 398
TYPE: PRT
ORGANISM: Homo sapiens
US-09-902-775A-84

Query Match      32.4%; Score 739; DB 4; Length 398;
Best Local Similarity 38.6%; Pred. No. 1.4e-56;
Matches 166; Conservative 73; Mismatches 147; Indels 44; Gaps 9;

QY 22 PGLRLRLLLLFSAALIPFG-----DGNLFTDVTVEGVAITISCOVNSKSDSVIQL 76
DB 4 PAASLLILLLLF-ACMAPEGANLSQDDSQFWISDETVAGGVVLCQVXKHEDSSLSQW 62
QY 77 LNPNGQITVFDPRPLKDSRFQLNFSSESLKXSLTNVSIISDEGRYFCQLYTDPPQESY 136

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DB 63 SNPAGQTLVFEKRALDNRIQLVTSRHELSTISISVALADEGETCSIFTPVPTAKS 122
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DB 123 LVTVGLIPKQRTIGVYSSIREKDTATLNQSSGSRPAALTRKQDQELHGPRTIQD 182
QY 186 SD--MYVTSQLMKVHKEDGVVICOVEHPAVTG-NLQTORVLEVOYKPCQVHIQMTVP 252
DB 183 PNGKFTVSSSVTFQVRRDDGASIVCSVHSESLKGDRETSQRIEVLVTPMIRPDP 242
QY 253 LOGLTREDALELCEALIGKPOPMVTVWAVDDEMQHVALSGPNLFINNKTNDGTR 312
DB 243 ---HPRBQKLLHCBERRGNVFPQYIMEX-BESVPELQYTESALIFPLNKSDSGTY 298
QY 313 CEASNIYKASDYMALVYDPPPTTPTTTTITTTTTITLITIDSRAGEGSIKAV 372
DB 299 CTATSNMGSYKAYVTLVNDPS---PVFSSSTY----- 329
QY 373 DHAVIGVAVVVPVAMCLIIIGRYPARHKGTVFTHKAGDADADATATINAGGON 432
DB 330 -HALLIGVAFVFLVLLMLFIHGYLIRKGYVLTBAGSDADADATATINAGGOS 388
QY 433 NSEKKEYFI 442
DB 389 GDDKKEYFI 398

RESULT 14
US-09-778-510-2
Sequence 2, Application US/09778510
Patent No. 6512095
GENERAL INFORMATION:
APPLICANT: Baum, Peter
TITLE OF INVENTION: Molecules Designated B7L1
FILE REFERENCE: 2844-US
CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: PCT/US99/17906
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: 60/095,663
PRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 432
TYPE: PRT
ORGANISM: Homo sapien
US-09-778-510-2

Query Match      31.6%; Score 722; DB 4; Length 432;
Best Local Similarity 36.4%; Pred. No. 4.9e-55;
Matches 169; Conservative 74; Mismatches 143; Indels 78; Gaps 11;

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DB 63 QDSQFWISDETVAGGVVLCQVXKHEDSSLSQWNSPAGQTLVFEKRALRNRIQLVTS 122
QY 103 SSSELKXSLTNVSIISDEGRYFCQLYTDPPQESYTTITVTVPPRNIMIDIOQDVAEGEI 162
DB 123 TPHELSTISISVALADEGETCSIFTPVPTAKSLVTVGLIPKQRTIGVYSSIREKDTA 182
QY 163 EVNCTAASAPATIRFKNTLKKR-SEVERMSD--MYVTSQLMKVHKEDGVVICOVE 219
DB 183 TLNQGSSGSRPAALTRKQDQELHGPRTIQDPRNGKFTVSSSVTFQVRRDDGASIV 242
QY 220 QVVEHPAVTG-NLQTORVLEVOYKPCQVHIQMTVPLOGLTREDALELCEALIGKPOPMV 278
DB 243 CSVHSESLKGDRETSQRIEVLVTPMIRPDP---HPRBQKLLHCBERRGNVFPQY 299

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QY 279 TWAVDEMPCHAVLGNLFNNLKTNDNGTYRCEASNIYKASHDYMLYVYDPTTIP 338
DB 300 LWK-EGSVPLKMQESALIFPLINKSDSGYGTATSNMGSYKAYTTLVNDPS--P 355
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DB 356 VSSSSSY-----HAIIGIVAFIVFLIMLIFLGHY 388
QY 399 FAHHKGYTFHEAKGADPAADATTAIINAEAGGONNSEKKEVEI 442
DB 389 LIRHKGTLTHEAKSDAPADPDIINAEAGGSGGDDKKEVEI 432

RESULT 15
US-09-205-258-947
; Sequence 947, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373

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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
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; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 947
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-205-258-947

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Query Match          14.7% Score 335; DB 4; Length 227;
Best Local Similarity 33.8%; Pred. No. 1,66-21;
Matches 78; Conservative 48; Mismatches 97; Indels 8; Gaps 5;

QY 106 ELKVLNVSISDEGRYFCQLYTDPPOSYTTITVLPBRLMTDIOQTAVEGEIEVN 165
DB 1 ELISISNVALADEGEYTCISFTWVETAKSIVTVLGIPKPIITGYKSLREKDTATLN 60

QY 166 CTAMASKPATITRMKGNTELKXK-SVEEWSQD--MYTVTSQMLKXKAKEDDGVVITQV 222
DB 61 CQSSGSKPARIITWKKSGQELHGEPTRIQEDPNKGTFTVSSVTFQVTRDGDASIVGCV 120

QY 223 EHPAVTG-NLQTORYLEVQYKPOVAHIQMTYPLQGLTRGDALELTCEAIGKQPMVTVW 281
DB 121 NHESLKGDARSTSGQIEVLYPTAMIRDPD---HPRRGQTLHCBGRGNFVQGYIME 177

QY 282 RVDDMPCHAVLGNLFNNLKTNDNGTYRCEASNIYKASHDYMLYVYD 332
DB 178 K-EGSVPLKMQESALIFPLINKSDSGYGTATSNMGSYKAYTTLVND 227

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Search completed: July 7, 2004, 06:05:18
Job time : 37.7688 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

CM protein - protein search, using sw model

Run on: July 7, 2004, 05:56:13 ; Search time 32.2751 Seconds

(without alignments)
1260.692 Million cell updates/sec

Title: US-10-622-237-4

Perfect score: 2197
Sequence: 1 AAPPGLRLRLLLLSAAL.....TAIINAGGQNNSEKKEYF 423

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	270	12.3	407	2 T08732	hypothetical prote
2	261.5	11.9	5175	2 T20992	hemipentameric prote
3	261.5	11.9	5198	2 T43290	poliovirus recepto
4	246.5	11.2	467	1 HLMSP3	poliovirus recepto
5	244	11.1	518	2 JC4024	poliovirus recepto
6	243	11.1	530	2 AS3437	poliovirus recepto
7	238.5	10.9	538	2 T68093	PRR2 delta - human
8	238	10.8	725	2 JEB0099	neural cell adhesi
9	237	10.8	417	2 A44194	poliovirus recepto
10	234.5	10.7	392	2 B44194	poliovirus recepto
11	234	10.7	1088	1 J1X1L1	neural cell adhesi
12	232.5	10.6	392	1 RMHUPD	poliovirus recepto
13	232.5	10.6	417	1 RMHUPD	poliovirus recepto
14	231	10.6	344	2 I56551	neurotrophin - rat
15	228.5	10.4	7962	2 T38346	elastic titin - hu
16	226	10.3	4162	2 T42633	connectin/citlin -
17	225	10.2	1011	2 T13669	neurexophilin - fr
18	222	10.1	725	2 JEB0100	neural cell adhesi
19	222	10.1	1092	1 JN0635	neural cell adhesi
20	220.5	10.0	338	2 JCS519	50K glycoprotein p
21	220	10.0	478	2 I53960	PRR2 alpha - human
22	217.5	9.9	345	2 S03199	opioid-binding pro
23	215.5	9.8	345	2 JC4025	opioid-binding cel
24	215.5	9.8	588	2 A45254	surface glycoprote
25	214	9.7	588	2 JH0506	adhesion molecule
26	212	9.6	4391	2 A38096	perlecan precursor
27	210.5	9.6	812	2 B42632	cell adhesion mole
28	210.5	9.6	932	2 A42632	cell adhesion mole
29	209.5	9.5	345	2 JCI239	opioid-binding pro

30	209.5	9.5	584	2 I50419	s-glycerin precurs
31	207.5	9.4	646	2 I38049	cell surface glyco
32	206.5	9.4	338	2 JC4776	limbic-system-asso
33	206.5	9.4	862	2 I49583	differentiation an
34	206.5	9.4	868	2 A46512	CD22 homolog/B lym
35	206	9.4	847	2 JH0371	B-cell adhesion pr
36	204	9.3	702	2 A36319	carcinoembryonic a
37	203.5	9.3	583	2 I39428	neogenin - chicken
38	202	9.2	1443	2 I50600	opioid-binding pro
39	200.5	9.1	338	2 JCI238	cell adhesion mole
40	200.5	9.1	755	2 C42632	DM-GRASP precursor
41	200	9.1	587	2 JH0464	heparan sulfate pr
42	197	9.0	3707	2 S18252	nephrin - human
43	196.5	8.9	1241	2 T37190	connectin 38 - chi
44	195	8.9	1323	2 PNC568	neural cell adhesi
45	193	8.8	761	1 JHUNG	

ALIGNMENTS

RESULT 1
T08732
hypothetical protein DKFP566B0846.1 - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
R/Octomwelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A/Reference number: Z15474
A/Accession: T08732
A/Molecule type: mRNA
A/Residues: 1-407 <OT>
A/Cross-references: EMBL:AL050071
A/Experimental source: fetal kidney; clone DKFP566B0846
C/Genetics:
A/Note: DKFP566B0846.1

Query Match 12.3%; Score 270; DB 2; Length 407;
Best Local Similarity 27.0%; Pred. No. 1.1e-11;

Matches 85; Conservative 58; Mismatches 124; Indels 48; Gaps 13;

QY	102	GRYFCOLYTD--POSSVYITIVLPVPRNLMIDIGKDAVEG--REIENVNCAASKPAT 157
DB	2	GKXICKATVFPFGNAGSSSTTVLVLPVPSLIK-GPDSLIDGNTVAICIAAGKPYA 60
QY	158	TTRFKNGKELKGSVEBWSDMY----TTSQMLKVKHEDDGPVICOYEHPAYTGN 212
DB	61	HIDW-EGD---LGEMESTTSPFNETATITISQYKLPTRPARGRITCVVKKHDLKND 114
QY	213	LGTQRYLEVQYKPOVHIGMTYDGLTREGDAFELTCALIGKPOVMTVWVRVDEMOH 272
DB	115	IYVSFTLIDQVAPESVVGYNWFWGRKG--VNKKCANADNPFPKSVWRSLDQWPDG 172
QY	273	AVLSEPNP-FINNLKNTNGTYRCEASNIIVGASHDVMYYVDDP--TTTP-----PTT 324
DB	173	LIASDNTLHFVHPLTFNYSGVYICKVNTSLGQRSDQKVIYISDPPTTTTLQPTIOMHST 232
QY	325	TTTTTTT-----TTTILITIDSAGEGRTIGADVAVIGVAVVFAVACLLI- 375
DB	233	ADIEPLATEPKLPPPLSTLATI-----KDTITATIASVVGALFIVASVLAGIFC 285
QY	376	-----ILGRYFARH 384
DB	286	YRRRTFRGDYFAKN 300

RESULT 2
T20992
hypothetical protein F1569.4a - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C/Accession: T20992; T24733

R: Sulston, J.
Submitted to the EMBL Data Library, December 1994
A: Reference number: Z19355
A: Accession: T20992
A: Status: preliminary; translated from GB/EMBL/DBD
A: Molecule type: DNA
A: Residues: 1-5175 <M12>
A: Cross-references: EMBL:Z47068; PIDN:CAA87335.1; GSPDB:GN00028; CESP:FL5G9.4a
A: Experimental source: clone F15G9
R: Kershaw, J.
Submitted to the EMBL Data Library, December 1994
A: Reference number: Z19929
A: Accession: T24734
A: Status: preliminary; translated from GB/EMBL/DBD
A: Molecule type: DNA
A: Residues: 1-5175 <M12>
A: Cross-references: EMBL:Z47070; PIDN:CAA87344.1; GSPDB:GN00028; CESP:FL5G9.4a
A: Experimental source: clone T09B9
C: Geneticks:
A: Gene: CESP:FL5G9.4a
A: Map position: X
A: Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;
A: Exons: 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1;
A: 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4879/1; 4941/1; 5011/1; 5077/1;
Query Match 11.9%; Score 261.5; DB 2; Length 5175;
Best Local Similarity 24.6%; Pred. No. 1.1e-09;
Matches 87; Conservative 65; Mismatches 130; Indels 71; Gaps 15;
Qy 34 VTVEGEVATISCCVNSDSDSVIQLNPNRQIYFRDFRL---KDSRFQNLNFSSEL 89
Db 2200 VTALKGALPFXCID--DDK---NFKQIILWNRVQIDLEADARITRL---SND 2249
Qy 90 KVSILTNVISDEGRYFCOLYTDPPQESYT-TITLVPRRLMDIQD-TAVGEIEVN 147
Db 2250 RLTIANTVNDGEGYSCRKXNDAGENSFDFKATLVPTTLMKDKKXKTAHSHSTVLS 2309
Qy 148 CTAAASKPATITIRPFKQ-----NKLKSKSEVEEWSMDVYTSQMLKVK 193
Db 2310 CPA-TGKREPITPFKQGEAHIENADIIENGLNG-----NQLKTRIK 2354
Qy 194 EDDGVPIVQVEHPAVTGNLQTORYLEYQKPOVH---IQMTYPLQGLTREGDAFELTCE 250
Db 2355 EGDGKTYTCEADNSA--GSVEODVNVVITIPKLEKDGIPSDYESQ---QNERVVISCP 2408
Qy 251 AIGKQPMVMTWVRVDEMPQHAVL---SGPNLFINNLTNGTYRCEASNIYGRAS 306
Db 2409 VYARP-PAKITWLAKGKPLQSDKFKVTSANGQKLYLFLKLETDSSKTCIAITNAGIDKR 2467
Qy 307 DYMALVYDPPTTTP-----PTTTTTTTTTTTTTTTTTDSRAGE 347
Db 2468 DFKVSMVAFPDEBNIVRITVNSGNPSTLHCPAKGSPSPITWLMKGNAIE 2520
RESULT 3
T43290
hemiceutin precursor - Caenorhabditis elegans
C: Species: Caenorhabditis elegans
C: Date: 11-Jan-2000 #sequence revision 11-Jan-2000 #text change 18-Feb-2000
C: Accession: T43290; T20993; T24734
R: Vogel, B.B.; Hedgecock, E.M.
Submitted to the EMBL Data Library, June 1996
A: Description: Hemiceutin is required for hemidesmosome mediated cell adhesion and germ
A: Reference number: Z22396
A: Accession: T43290
A: Molecule type: RNA
A: Status: preliminary; translated from GB/EMBL/DBD
A: Residues: 1-5198 <VOG>
A: Cross-references: EMBL:AF074901; PIDN:AA02792.1
R: Sulston, J.
Submitted to the EMBL Data Library, December 1994
A: Reference number: Z19355
A: Accession: T20993

A: Status: preliminary; translated from GB/EMBL/DBD
A: Molecule type: DNA
A: Residues: 1-5198 <M12>
A: Cross-references: EMBL:Z47068; PIDN:CAA87336.1; GSPDB:GN00028; CESP:FL5G9.4b
A: Experimental source: clone F15G9
R: Kershaw, J.
Submitted to the EMBL Data Library, December 1994
A: Reference number: Z19929
A: Accession: T24734
A: Status: preliminary; translated from GB/EMBL/DBD
A: Molecule type: DNA
A: Residues: 1-5198 <M12>
A: Cross-references: EMBL:Z47070; PIDN:CAA87345.1; GSPDB:GN00028; CESP:FL5G9.4b
A: Experimental source: clone T09B9
C: Geneticks:
A: Gene: hlm-4; F15G9.4b
A: Map position: X
A: Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;
A: Exons: 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1;
A: 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 5100/1;
Query Match 11.9%; Score 261.5; DB 2; Length 5198;
Best Local Similarity 24.6%; Pred. No. 1.1e-09;
Matches 87; Conservative 65; Mismatches 130; Indels 71; Gaps 15;
Qy 34 VTVEGEVATISCCVNSDSDSVIQLNPNRQIYFRDFRL---KDSRFQNLNFSSEL 89
Db 2200 VTALKGALPFXCID--DDK---NFKQIILWNRVQIDLEADARITRL---SND 2249
Qy 90 KVSILTNVISDEGRYFCOLYTDPPQESYT-TITLVPRRLMDIQD-TAVGEIEVN 147
Db 2250 RLTIANTVNDGEGYSCRKXNDAGENSFDFKATLVPTTLMKDKKXKTAHSHSTVLS 2309
Qy 148 CTAAASKPATITIRPFKQ-----NKLKSKSEVEEWSMDVYTSQMLKVK 193
Db 2310 CPA-TGKREPITPFKQGEAHIENADIIENGLNG-----NQLKTRIK 2354
Qy 194 EDDGVPIVQVEHPAVTGNLQTORYLEYQKPOVH---IQMTYPLQGLTREGDAFELTCE 250
Db 2355 EGDGKTYTCEADNSA--GSVEODVNVVITIPKLEKDGIPSDYESQ---QNERVVISCP 2408
Qy 251 AIGKQPMVMTWVRVDEMPQHAVL---SGPNLFINNLTNGTYRCEASNIYGRAS 306
Db 2409 VYARP-PAKITWLAKGKPLQSDKFKVTSANGQKLYLFLKLETDSSKTCIAITNAGIDKR 2467
Qy 307 DYMALVYDPPTTTP-----PTTTTTTTTTTTTTTTTTDSRAGE 347
Db 2468 DFKVSMVAFPDEBNIVRITVNSGNPSTLHCPAKGSPSPITWLMKGNAIE 2520
RESULT 4
HIMSP3
poliovirus receptor homolog precursor - mouse
C: Species: Mus musculus domesticus (western European house mouse)
C: Date: 30-Jun-1993 #sequence revision 30-Jun-1993 #text change 22-Jun-1999
C: Accession: A38211
R: Morrison, M.R.; Raccanelli, V.R.
J. Virol. 66, 2807-2813, 1992
A: Title: Molecular cloning and expression of a murine homolog of the human poliovirus re
A: Reference number: A38211; MUID:92219365; PMID:1560525
A: Accession: A38211
A: Molecule type: DNA
A: Residues: 1-467 <MOR>
A: Cross-references: GB:M80206; MUID:9199785; PIDN:AAA39734.1; PID:9199786
A: Superfamily: poliovirus receptor; immunoglobulin homology
C: Keywords: duplication; glycoprotein; transmembrane protein
F: 1-25/Domain: signal sequence #status predicted <Sig>
F: 26-467/Product: poliovirus receptor homolog #status predicted <EXT>
F: 26-354/Domain: extracellular #status predicted
F: 47-133/Domain: immunoglobulin homology <IMM1>
F: 167-231/Domain: immunoglobulin homology <IMM2>
F: 267-322/Domain: immunoglobulin homology <IMM3>
F: 355-374/Domain: transmembrane #status predicted <IMM>

F:375-467/Domain: intracellular #status predicted <INT>
 F:54-131,174-229,274-320/Dissulfide bonds: #status predicted
 F:128,138,315/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 11.2%; Score 246.5; DB 1; Length 467;
 Best Local Similarity 21.6%; Pred. No. 6e-10; Mismatches 196; Indels 99; Gaps 16;

Matches 101; Conservative 72; Mismatches 196; Indels 99; Gaps 16;

```

QY 4 PGLRLRLLLLSAALIPFGDQNLFTKDVVIEGEV---ATISQV-----48
DB 14 PTLPLPLPLLL---LQETG-AQDVRAVLPEVAGRLGIVELPCHLLPTTERVSGVT 68
QY 49 -NKSDSVYIQLNPNKQTIYFRDFRPLKDSRFQ-----LNFSSSELKVSILTVNSIS 99
DB 69 WQRLDGTVAAPFHS---FGVDFPNSQFSKDRLSFYARPEPTNADLNDATLAFGLAVE 124
QY 100 DEGRYFCQLYTDP--PQESYTTITVLVPPRLMIDIQDITAVEGEIEV-----NCT 149
DB 125 DEGNVTCEPATFPNGTRRGVTLKRLIAPEN-----HAHQVLTIGQSVAVARCV 175
QY 150 AMASRPATTIRWFKG-NKELKGSVEEWSMDYTVTSQMLKVHKEDDGVPTICQVEHPA 208
DB 176 STGGPAPRITWISLIGGEADTQEPGLOAGTVTIISRYSLVPYGRADGVATCRVHES 235
QY 209 VTGNLQTRVLEVOYKQPVNIQMTYPLQGLTREGDAFELTCEALGKQPVWTVWRVDE 266
DB 236 FEEPIILPVTLISVRYPEVVIS-GYDDNWYIGRSEAL-LTCDVANSNEPPTIDYDKSTSGV 293
QY 269 MPQHAVLSGPNLFNNLKNKTNGTYRCEASNIVGKASDVMLYVYDPTTIPPTTTT 328
DB 294 FPASAVAGSQLVHSVDRMNTTTFICTATNAVGTGRAEQVILVRDTPQA-----343
QY 329 TTTTTLTTLITTSRAGEEGTIGAVDHAIVGVAVVVR--WLCILIIIGRYFAHKG 366
DB 344 -----SR-----DVGPLWGAAGVGLTLLVLLAGGFLAILLGRRRRSPG 384
QY 387 TYFTHAKGADDA-----ADADTAIINAGGQNNSEKKE 421
DB 385 GGGNDGGRGSYDPKTYQVNGGPFVFWMSASPEPRPRPGREDEDEEEB 432

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RESULT 5

poliovirus receptor-related protein precursor - human
 C/Species: Homo sapiens (man)
 C/Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Nov-1999
 C/Accession: J04024
 R/Lopez, M.; Eberle, F.; Mattei, M.G.; Gabert, J.; Birg, F.; Bardin, F.; Maroc, C.; Dubr
 Gene 155, 261-265, 1995
 A/Title: Complementary DNA characterization and chromosomal localization of a human gene
 A/Reference number: J04024; MUID:95237621; PMID:7721102
 A/Accession: J04024
 A/Molecule type: mRNA
 A/Residues: 1-518 <LOP>
 A/Cross-references: EMBL:X76400; NID:9732795; PIDN:CAA53960.1; PID:9732796
 C/Genetics:
 A/Gene: GDB:PVPR1
 A/Cross-references: GDB:583951
 A/Map position: 11q23-11q24
 C/Superfamily: poliovirus receptor; immunoglobulin homology
 C/Keywords: glycoprotein; transmembrane protein
 F:130/Domain: signal sequence #status predicted <SIG>
 F:31518/Product: poliovirus receptor-related protein #status predicted <MAT>
 F:356-379/Domain: transmembrane #status predicted <TM>
 F:36,72,82,139,287,308,333/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 11.1%; Score 244; DB 2; Length 518;
 Best Local Similarity 25.1%; Pred. No. 1e-09;

Matches 104; Conservative 59; Mismatches 155; Indels 96; Gaps 20;

```

QY 56 IQLNPNKQTIYFRDFRPLKDSRFQNLNFSSELKVSILTVNSISDEGRYFCQLYTDP--113
DB 78 VAINPBMGVSVLAPYR-----ERVAFLRPSFTDGTLSRLLEDEEGVTCBPATPTGN 133

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QY 114 QESYTTITVLVPPRLMIDIQDITAVEGEIEV---NCTAMASRPATTIRWFKGNKELK 169
DB 134 RESQMLITWAKRPTNMIIEGQAVLRAKQGDQDRVLVATCTSANGKRPSSVSN---ETRLK 190
QY 170 GKSEV--EEMSDN--YTTSQMLKVHKEDDGVPTICQVEHPAVTGNLQTRY-----LE 220
DB 191 GEARVPDSDGTPMAPVTVISRYELVPSREAHQOQSLACIV-----NYHDFKESLTLN 243
QY 221 VOYKQPVNIQ---MTVPLQGLTREGDAFELTCEALGKQPVWTVWRVDEMPQHAVLSG 277
DB 244 VOIEPEVTIIEGFGNWTYLRMD-----VKLTCAADNPATBYHMTLNGSLPKVGEAON 298
QY 278 PNLFINN-LNKTDNGTYRCEASNIVGKASDVMLYVYDPTTIPPTTTT 336
DB 299 RTLFFGAPINYSLAGYICEATNPIDTRSGQVEVNTERTPPSP-----344
QY 337 LTIITSRAGEEG-TIGAVDHAIVGVAVVVR--WLCILIIIGRYFA---RH--KGYTF 389
DB 345 -----EGRRAPVPPTALIGVAGSI---LVLIVGGIIVALLRRRHTFGDYS 391
QY 390 T-----HEAKGA-----DPAADATAIINAGGQNNSEKKE 421
DB 392 TKKHVVGNGSKAGIQHHPRPAQNLQYRDDSDDEKKA--GLGGSYEEBEEB 443

```

RESULT 6

poliovirus receptor mpvr - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
 C/Accession: A53437
 R/Aoki, U.; Koike, S.; Ise, I.; Sato-Yoshida, Y.; Nomoto, A.
 J. Biol. Chem. 269, 8431-8438, 1994
 A/Title: Amino acid residues on human poliovirus receptor involved in interaction with
 A/Reference number: A53437; MUID:94179228; PMID:8132669
 A/Accession: A53437
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-530 <NOK>
 A/Cross-references: GB:ID26107; NID:9475017; PIDN:BA05103.1; PID:9825507
 A/Experimental source: C57/BL6, brain
 A/Note: sequence extracted from NCBI backbone (NCBIN:146664, NCBI:146667)
 C/Superfamily: poliovirus receptor; immunoglobulin homology
 F:47-133/Domain: immunoglobulin homology <IM>

Query Match 11.1%; Score 243; DB 2; Length 530;
 Best Local Similarity 22.6%; Pred. No. 1.2e-09;

Matches 90; Conservative 61; Mismatches 162; Indels 86; Gaps 14;

```

QY 4 PGLRLRLLLLSAALIPFGDQNLFTKDVVIEGEV---ATISQV-----48
DB 14 PTLPLPLPLLL---LQETG-AQDVRAVLPEVAGRLGIVELPCHLLPTTERVSGVT 68
QY 49 -NKSDSVYIQLNPNKQTIYFRDFRPLKDSRFQ-----LNFSSSELKVSILTVNSIS 99
DB 69 WQRLDGTVAAPFHS---FGVDFPNSQFSKDRLSFYARPEPTNADLNDATLAFGLAVE 124
QY 100 DEGRYFCQLYTDP--PQESYTTITVLVPPRLMIDIQDITAVEGEIEV-----NCT 149
DB 125 DEGNVTCEPATFPNGTRRGVTLKRLIAPEN-----HAHQVLTIGQSVAVARCV 175
QY 150 AMASRPATTIRWFKG-NKELKGSVEEWSMDYTVTSQMLKVHKEDDGVPTICQVEHPA 208
DB 176 STGGPAPRITWISLIGGEADTQEPGLOAGTVTIISRYSLVPYGRADGVATCRVHES 235
QY 209 VTGNLQTRVLEVOYKQPVNIQMTYPLQGLTREGDAFELTCEALGKQPVWTVWRVDE 268
DB 236 FEEPIILPVTLISVRYPEVVIS-GYDDNWYIGRSEAL-LTCDVANSNEPPTIDYDKSTSGV 293
QY 269 MPQHAVLSGPNLFNNLKNKTNGTYRCEASNIVGKASDVMLYVYDPTTIPPTTTT 328
DB 294 FPASAVAGSQLVHSVDRMNTTTFICTATNAVGTGRAEQVILVRDTPQA-----343

```

Oy 329 TTTTTLITITDSRAGEGTIGAVDHAVIGVAVV 367
 Db 344 -----AGAGATGG-----ITGGIATAT 361

RESULT 7

168093
 PRR2 delta - human
 C:Species: Homo sapiens (man)
 C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000
 C:Accession: 168093
 R:Berle, F.; Dubreuil, P.; Mattei, M.G.; Devillard, E.; Lopez, M.
 Gene 159, 267-272, 1995
 A:Title: The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is th
 A:Reference number: 153960; MUID:95347610; PMID:7622062
 A:Accession: 168093
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-538 <RES>
 A:Cross-references: GB:579172; NID:g1042204; PID:g1042205
 C:Genetics:
 A:Gene: PRR2delta
 C:Superfamily: poliovirus receptor; immunoglobulin homology
 F:276-331/Domain: immunoglobulin homology <IMM>

Query Match 10.8%; Score 238.5; DB 2; Length 538;

Best Local Similarity 22.8%; Pred. No. 2, 6e-09; Mismatches 196; Indels 113; Gaps 17;

Matches 110; Conservative 63; Mismatches 196; Indels 113; Gaps 17;

Oy 2 APPGLRLILLILLSAALIPGDCQNLFTKDVVIEGEVATISCVNKSDDSVIQLNP 61
 Db 12 SPFLPLMLPILL-----LLETG-AQDVRYQVLPEVRG-----QLGTVELPCILLP 59
 Oy 62 -----NRQTYFRDPRPKDSRF-----QLNFSSS----- 87
 Db 60 VPGYISLVWQRPDAFANQNV--AAFHPRMGSPSPKRGSERLSPVSAKOSTGQDTE 117
 Oy 88 -----ELKVSILNVSISDEGRYFCQLYTD--POESYTTITVLVPPRLMIDIQKTAVEG 141
 Db 118 AELQDATTALHGLVEDEGNITCEFATFPKGSVRGTMWLVIAKPKA-QAEAGKATPFSQD 176
 Oy 142 EEIEVNCITANASKPATIRWFKQ-NKELKGSVEEMSDMTVTYSQMLKVKHEDGPVY 200
 Db 177 PTVALCISKRGPRPARISWLSLDMWAKETQVSGTAGVTVTSRPTLVPSGRADGVTV 236
 Oy 201 ICQVHNATVGNLTQRYLEVQYKQVHIQMTYPLQGLTRGDAFELTCALIKPQVWV 260
 Db 237 TCKVHESFEPPALIPVTLVRYPEVVIS-GIDDMVLCRTD--TLSCDVRSNPEPTG 294
 Oy 261 TWVVDDEMPQHAVLSGPNLFINNKTNDGTYSCEASNIVGKAHSDMYLVYDPTTIP 320
 Db 295 DMSITSGTFPSAQAQSQVLIVHVDLFTTTPCTVTNAGVGRAGQVIFVRETN-- 352
 Oy 321 PPTTTTTTTTTTTTTLITITDSRAGEGTIGAVDHAVIGVAVVFAFMCILILIGR 380
 Db 353 -----AGAGATGG-----ITGGIATATATAAATGILICR 383
 Oy 381 FARHGTFTBAKGAADDAAD-----TAIINAE-----GGONNSEKKE 421
 Db 384 QQRKEQT-----LOGAEEDDLBGRPSYKPTPRKAKLEADMPQLFTLGASHSPKTP 438
 Oy 422 YF 423
 Db 439 YF 440

RESULT 8

JE0099
 neutral cell adhesion molecule 1 - African clawed frog
 N:Alternate names: N-CAM 1
 C:Species: Xenopus laevis (African clawed frog)
 C>Date: 19-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000

C:Accession: JE0099
 R:Kudo, M.; Takayama, T.; Shikawa, K.
 Biochem. Biophys. Res. Commun. 245, 127-132, 1998
 A:Title: Molecular cloning of ssd-form neutral cell adhesion molecules (N-CAMs) as the ma
 A:Reference number: JE0099; MUID:98204770; PMID:9553795
 A:Accession: JE0099

A:Molecule type: mRNA

A:Residues: 1-725 <KID>

A:Cross-references: DBJ:AB008162; NID:g3116226; PID:NBA25931.1; PID:g3116227

A:Experimental source: heart

C:Comment: This protein mediates and regulates various cell-cell interactions through bo

C:Superfamily: neutral cell adhesion molecule; fibronectin type III repeat homology; immu

F:413-475/Domain: immunoglobulin homology <IMM>

F:512-589/Domain: fibronectin type III repeat homology <3FR>

Query Match 10.8%; Score 238; DB 2; Length 725;

Best Local Similarity 26.2%; Pred. No. 4, 2e-09; Mismatches 148; Indels 42; Gaps 15;

Matches 89; Conservative 61; Mismatches 148; Indels 42; Gaps 15;

Oy 32 KDVTVIEGEVATISC---QVN---KSDDSVITQLN---PNRQTYFRDPRPKDSRFOL 81
 Db 139 KDQYIVVNPPTIQARQLRVNATKMAESVLSGDADGFPDPELSWIKKEPIEDGB-EX 257
 Oy 82 LNFSSSELKVSILNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRLMIDIQKTAVEG 141
 Db 258 ISFNEDQSEMTIHVEXKDEAEVSC-IANNQAGEAEATILLKYAKEXKITVVENKTAVEL 316
 Oy 142 EEIEVNCITANASKPATIRWFKQK-----LKGSVEEMSDMTVTYSQMLKVKHKE 194
 Db 317 DEITLTCEA-SGDIPSLTMTAVRANISSEKTTIDGHIYKHEIRM-----SALTLDIQY 371
 Oy 195 DDGVFVICOVHPAVTGNLTQRYLEVQYKQVHIQMTYPLQGLTRGDAFELTCALIK 254
 Db 372 TDAGEYFCIANP-IGVDMQAM-YFEVQYAPKIR-----GPVAVYTWEGNPNVITCEVFAH 425
 Oy 255 PQVWVTVTRVDDMPQH-----AVLSGP---NFINNKTNDGTYSCEASNIVGKAH 306
 Db 426 PR-AAVTFWRDQQLPSSNFENIKYVSGPSSSLAEVPSDNDGNYNCTALINTIGHEFS 484
 Oy 307 DMYLVYDPTTIPPTTTTTTTTTTTTTTTTTTTTTITITDSRAG 346
 Db 485 ERLVQADTPSS---PARKKEPYSSTVWVTFDEPDSFGG 521

RESULT 9

A44194

poliovirus receptor (clone AGM-alpha-1) - green monkey

C:Species: Cercopithecus aethiops (green monkey, grivet)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C:Accession: A44194

R:Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.

J. Virol. 66, 7059-7066, 1992

A:Title: A second gene for the African green monkey poliovirus receptor that has no puta

A:Reference number: A44194; MUID:93059651; PMID:1331508

A:Accession: A44194

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-417 <KOI>

A:Cross-references: GB:S48777

C:Superfamily: poliovirus receptor; immunoglobulin homology

C:Keywords: transmembrane protein

F:259-314/Domain: immunoglobulin homology <IMM>

Query Match 10.8%; Score 237; DB 2; Length 417;

Best Local Similarity 23.8%; Pred. No. 2, 4e-09; Mismatches 194; Indels 80; Gaps 18;

Matches 107; Conservative 68; Mismatches 194; Indels 80; Gaps 18;

Oy 1 AAPGLRLILLILLSAALIPGDCQNLFTKDVV--IEGEVATISC--OVNKSDDSVI 56
 Db 8 ANFP-----LLTLLLELSWPPPGDIIIVAPQVPEFLDSTVLPCTVQVPGMEETHV 61
 Oy 57 QLNNR-----QTYFRDPRPKDSRFQLNFSSELKVSILNVS-----ISDEGRY 104

Db 62 SOLTWSRHGSGSMAVHQTGPNYSEPRLEFVARLCTELRDASLMFGRLVDEGNY 121
QY 105 FQOLYVDPQESYTT---ITVYVPRNLMIDIOKTPAVEGEIEY-NCTAMASKPATIR 160
Db 122 TC-LFTVTFPGQSGSRVDIMRLVAKPQN-TAEVOK-VOLTGKVPVARSCTGGRPAHIT 178
QY 161 WFKGNKELKGRSEVE---WSDMTVTYSQMLKTKHKKEDDGPVVCQVEHPAVTGNLTQ 216
Db 179 W---HSDLGMPNTOQABGFLSGYTVTSMLTVLSSQVDGKSVTCYKHEHSEFKPQLTT 235
QY 217 RYLEYQYKPOVHIQMTYPLQGLTRGDAFELTCEAIGKQPVMVTWVRVDEMPQAVLS 276
Db 236 VMLTYVYPPPEVVIS-GYDNMWTLSQNEA-TLTCARSNBEPFGYMWSTTGGPLPFAVAQ 293
QY 277 GPNLNNLKTNDCTYCEASNIYKAKHSDMYVYVPPPTIIPPTTTTTTTTTTTTT 336
Db 294 GAQLIRPVDKPINTTFICNVTNALGARQAEITVQVKEGPSEPS----- 338
QY 337 LTIITDSRAGEGTIGAVDHAIVGVAVVFMCLIIILGRYPARKGT---YFTHE 392
Db 339 -----GMSNNIIFILIGIVI---LTLTIGIVYFRRCRREFIMCHL 380
QY 393 AKGADADADADTAITNABGQNNSEKKE 421
Db 381 SPSSEHSA-----SANGYISYSDVSR 404

RESULT 10

B44194
poliovirus receptor (clone AGM-delta-1) - green monkey
C/Species: Cercopithecus aethiops (green monkey, givvet)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C/Accession: B44194
R/Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.
J. Virol. 66, 7059-7066, 1992
A/Title: A second gene for the African green monkey poliovirus receptor that has no putative reference number: A44194; MUID:93059651; PMID:1331508
A/Accession: B44194
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-392 <KOI>
A/Cross-references: GB:S48817
C/Superfamily: poliovirus receptor; immunoglobulin homology
F:259-314/Domain: immunoglobulin homology <IMM>

Query Match 10.7%; Score 234.5; DB 2; Length 392;
Best Local Similarity 24.4%; Pred. No. 3.4e-09;

Matches 100; Conservative 58; Mismatches 180; Indels 71; Gaps 16;

QY 1 AAPGLRLRLILLLISAALIFTDGQNLFTKQVY--TEGEVATISC--QVNSKSDSVI 56
Db 8 AMP-----LTLTLELSWPPPGTGDIIVQAPQVPGFLDVSYTLPCYIQVPMGEETHV 61
QY 57 QLANENR-----QTIYFRDPRPLKDSRFQLNFSSELKVSILTVNS-----ISDEGRY 104
Db 62 SOLTWSRHGSGSMAVHQTGPNYSEPRLEFVARLCTELRDASLMFGRLVDEGNY 121
QY 105 FQOLYVDPQESYTT---ITVYVPRNLMIDIOKTPAVEGEIEY-NCTAMASKPATIR 160
Db 122 TC-LFTVTFPGQSGSRVDIMRLVAKPQN-TAEVOK-VOLTGKVPVARSCTGGRPAHIT 178
QY 161 WFKGNKELKGRSEVE---WSDMTVTYSQMLKTKHKKEDDGPVVCQVEHPAVTGNLTQ 216
Db 179 W---HSDLGMPNTOQABGFLSGYTVTSMLTVLSSQVDGKSVTCYKHEHSEFKPQLTT 235
QY 217 RYLEYQYKPOVHIQMTYPLQGLTRGDAFELTCEAIGKQPVMVTWVRVDEMPQAVLS 276
Db 236 VMLTYVYPPPEVVIS-GYDNMWTLSQNEA-TLTCARSNBEPFGYMWSTTGGPLPFAVAQ 293
QY 277 GPNLNNLKTNDCTYCEASNIYKAKHSDMYVYVPPPTIIPPTTTTTTTTTTTTTTTT 336
Db 294 GAQLIRPVDKPINTTFICNVTNALGARQAEITVQVKEGPSEPS----- 338

QY 337 LTIITDSRAGEGTIGAVDHAIVGVAVVFMCLIIILGRYPARKGT 385
Db 339 -----GMSNNIIFILIGIVI---LTLTIGIVYFRSR 369

RESULT 11

neural cell adhesion molecule long domain form precursor - African clawed frog
N/Alternate names: NCAM-180
N/Contains: neural cell adhesion molecule, short domain form (NCAM-140)
C/Species: Xenopus laevis (African clawed frog)
C/Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 22-Jun-1999
C/Accession: S09600
R/Krieg, P.A.; Sakaguchi, D.S.; Kintner, C.R.
Nucleic Acids Res. 17, 10321-10335, 1989
A/Title: Primary structure and developmental expression of a large cytoplasmic domain of NCAM
A/Reference number: S09600; MUID:90098871; PMID:2481269
A/Accession: S09600
A/Molecule type: mRNA
A/Residues: 1-1088 <XRI>
A/Cross-references: EMBL:M5696; NID:g214609; PID:AAA49909.1; PID:g214610
A/Note: the authors translated the codon AAA for residue 970 as Leu
C/Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mc
C/Genetics: Several forms of NCAM are produced by alternative splicing.
A/Genes: NCAM

C/Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immunoglobulin homology
C/Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; signal sequence
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-1088/Product: neural cell adhesion molecule, long domain form #status predicted <L>
F:20-803,1050-1088/Product: neural cell adhesion molecule, short domain form #status predicted <EXT>
F:23-95/Domain: extracellular #status predicted <EXT>
F:129-188/Domain: immunoglobulin homology <IMM>
F:149-153/Region: heparin binding #status predicted
F:158-162/Region: heparin binding #status predicted
F:225-284/Domain: immunoglobulin homology <IMM>
F:317-381/Domain: immunoglobulin homology <IMM>
F:413-475/Domain: immunoglobulin homology <IMM>
F:512-569/Domain: fibronectin type III repeat homology <FN3>
F:618-679/Domain: fibronectin type III repeat homology <FN3>
F:706-723/Domain: fibronectin type III repeat homology <FN3>
F:724-1088/Domain: intracellular #status predicted <INT>
F:41-93,136-186,232-282,323-379,420-473/Disulfide bonds: #status predicted
F:219,310,341,417,443,472/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.7%; Score 234; DB 1; Length 1088;
Best Local Similarity 25.9%; Pred. No. 1.3e-08;

Matches 88; Conservative 62; Mismatches 148; Indels 42; Gaps 15;

QY 32 KDVTVEGEVATISC---QVNSKSDSVI-----PNQTIYFRDPRPLKDSRFQL 81
Db 199 KDQIVLVNVPPTIQARQLVATNANASVVLSCADGPRDEISLTKGGEIIDE-EK 257
QY 82 LNFSSSELKVSILTVNSISDEGRFQLYTDPQESTTTITVYVPRNLMIDIOKTPAVG 141
Db 258 ISFNEQSEMTIHHVKKDDEAEVSC-IANNQGEAATILKLYAPKITYENKTAVAL 316
QY 142 EEEVENCAMASKPATIRIFPKGNK-----LKKSEVEEMSDYVTSQMLKVNHE 194
Db 317 DEITLICEA-SGPRISITMTRAVRNISEATLDOHIVYKHIR-----SALTLDIOY 371
QY 195 DQGVPIVCQVEHPAVTGNLTQRYLEVQYKPOVHIQMTYPLQGLTRGDAFELTCEAIGK 254
Db 372 TDAGEYFCIASNP-IGVDQAM-YEVQYAPKIR-----GPVVVYTWEGPNVITCEVFAH 425
QY 255 PCPVMTVYVRVDEMPQAVLS-----AVISGP---NLFINNKTNDCTYCEASNIYKAKH 306
Db 426 PR-AATVTRDQQLBSSNFSNIKIYSGPTSSLEVNDSLENDPFGYNCTAINTIGHERS 484
QY 307 DVMVYVDPPTIIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 346
Db 485 EFTLVQADTPSS---PAIRKVEPVSSTWIVDEPDSITG 521

Db 242 YPEPVSIS-GYDNMTLGONEA-TLTCDARSNPEPTGYNWSTTWGPPLPPFAVAGAOGLLI 299
 QY 283 NNINKTNDCTYCEASNIYGAHSDYMLVYDPPTTPTTTTITTTTITTTITTD 342
 Db 300 RPVDKRNITTLICVNTNALGARQAEITVQKE-----GPPSHS----- 338
 QY 343 SRAGEGTGAVDHAIVGVAVVVFAMCLIIIGRTF 381
 Db 339 -----GMSRNATITLVIGLIVF---LTLIGIGIVF 365

RESULT 14

neurotrophin - rat
 156551
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
 C:Accession: 156551
 R:Struyk, A.F.; Canoll, P.D.; Wolfgang, M.J.; Rosen, C.L.; D'Eustachio, P.; Salzer, J.L.
 J. Neurosci. 15, 2141-2156, 1995
 A:Title: Cloning of neurotrophin defines a new subfamily of differentially expressed neur
 A:Reference number: 156551; MUID:95198094; PMID:7891157
 A:Accession: 156551
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-344 <RES>
 A:Cross-references: EMBL:U16845; NID:G755184; PIND:AA67445.1; PID:G755185
 C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi

Query Match 10.5%; Score 231; DB 2; Length 344;
 Best Local Similarity 26.2%; Pred. No. 5,1e-09;

Matches 85; Conservative 56; Mismatches 134; Indels 50; Gaps 15;

QY 10 LLLLLSAALIPFG-----DQGNLFTK---DYTVGEVATISQVNSKSDSVYQLNPN 62
 Db 14 LVVSLRLFLVPTVPVPSGDAITPKAMDNVTAQGSATLRTCT--DNKRVTVAMLN 70
 QY 63 RQTI-YFRDFRPLKDSRFLNFSSELKSLTNVSISEGRYFCQLYTD-PPOESYTTI 120
 Db 71 RSTILYAGNDKWCIDPRVLLSNQTQYSIEIQNDVDYDEGRYCSVOTDNHPRKSRVHL 130
 QY 121 TVLVPRRLMIDIOQDTAV-EGEIEVNCTAMASKPATITRMFKGNKELKSGSEVEKSD 179
 Db 131 IVQVSPK--IVEISSDISINEGNNISLTCLIA-TGRPEPTVTMRHISPKAVGVSEDEYLE 187
 QY 180 MYTVTSQMLKVH---KEDDGVPIVLCQYEHPAVTGNLQTRYLEVOYKPOVHIQMTYPLQ 236
 Db 188 IGGITREOSGHEGASNDVAAPVRRVN-----VTVNIPIYIS-----EAK 229
 QY 237 GL-TREGAFELTCEAIKPPQVMTVTVRVDDEMPQ-----HAVLSGNLFINNLN 286
 Db 230 GTGVFVGQKQTLQCEASAVPS-AEFQMFKDKRLVEGKGVKVENRPPLSRLTFP--NVS 286
 QY 287 KTDNGTYRCEASNIYGAHSDYMLY 311
 Db 287 EHDYGNITCVASNKLGHNASIMLF 311

RESULT 15

138346
 elastic titin - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
 C:Accession: 138346
 R:Labelle, S.; Kolmerer, B.
 Science 270, 293-296, 1995
 A:Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.
 A:Reference number: A57430; MUID:96026330; PMID:7569978
 A:Accession: 138346
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-7962 <RES>
 A:Cross-references: EMBL:X90569; NID:G1017426; PIND:CAA62189.1; PID:G1017427
 C:Genetics:

A:Gene: GDB:TTN
 A:Cross-references: GDB:127867; OMIM:188840
 A:Map position: 2q31-2q31

Query Match 10.4%; Score 228.5; DB 2; Length 7962;
 Best Local Similarity 26.1%; Pred. No. 4e-07;
 Matches 80; Conservative 55; Mismatches 130; Indels 41; Gaps 13;

QY 35 TVIEGEVATISQVNSKSDSVIO---LNL-----PNRQTIYFRDPRPLKDSRFQNLNF 84
 Db 770 TVLDRIAPFTPTPLKRVDSVANGTCRLDCKINGSLPMKVS-WFKDGEIAPSDRRIRAF 828
 QY 85 SSELKSLTNVSISEGRYFCQLYTD-PPOESYTTITVLVPPRNIMIDIOQDTAVEGE 143
 Db 829 VEGTASLEIRVMDNDAGNFTCRATNSVSGSKSSGALIVQEPSPFTKPGSKD-VLPGSA 887
 QY 144 IEVNCTAMASKPATITRMFKGNKELG-----KSEVEKSDMYTVTSQMLKVHKKEDD 196
 Db 888 VCLKSTFGSTP-LTRKMFKNKELVSGSCYITKEALBSLELYLV-----KTSQ 937
 QY 197 GVPVLCQYEHPAVTGNLQTRYLEVOYKPOVHIQMTYPLQGLTRGDAFELTCEAIKGPQ 256
 Db 938 SGTYTCVSN--VAGGVCSANLFVK-EPATTFEKLEPQ-LKKGDATQLAKVTGTP- 992
 QY 257 PVAWTVTVRVDDEMPQHA-----VLSGNLFINNLKTDNGTYRCEASNIYGAHSDYML 310
 Db 993 PKITWFAANDREIKESSKHMSFVESTAVLRITLDVGIEDSGEYWCRAQNEAGSDHCSSIV 1052
 QY 311 YVYDPP 316
 Db 1053 IVKESP 1058

Search completed: July 7, 2004, 06:00:28
 Job time: 33.2751 secs

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CM protein - protein search, using sw model

Run on: July 7, 2004, 05:56:13 ; Search time 27.874 seconds

(without alignments)
790,187 Million cell updates/sec

Title: US-10-622-237-4

Perfect score: 2197

Sequence: 1 AAPPGLRLRLILILISAAAL.....TAIINAGGQNNSEKKEYP 423

Scoring table: BLOSUM62

Searched: 141681 segs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_42:*

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	229.5	11.8	515	1	Q9G176 sus scrofa
2	252.5	11.5	517	1	PVR1_PIG
3	243	11.1	530	1	PVR2_MOUSE
4	238.5	10.9	538	1	PVR2_HUMAN
5	237	10.8	417	1	PVR_CERAE
6	236	10.7	515	1	PVR1_MOUSE
7	234	10.7	1088	1	NCA1_XENLA
8	232	10.6	344	1	NTR1_MOUSE
9	231.5	10.5	417	1	PVR_HUMAN
10	231	10.5	344	1	NTR1_RAT
11	229	10.4	344	1	NTR1_HUMAN
12	225.5	10.3	837	1	NCM2_MOUSE
13	222	10.1	837	1	NCM2_HUMAN
14	222	10.1	1092	1	NCA2_XENLA
15	221	10.1	1242	1	NPHN_MOUSE
16	220.5	10.0	338	1	LAMP_CHICK
17	220	10.0	337	1	OPCM_CHICK
18	218	9.9	583	1	C166_MOUSE
19	217.5	9.9	345	1	OPCM_BOVIN
20	215.5	9.7	345	1	OPCM_HUMAN
21	214	9.7	588	1	C166_CHICK
22	211	9.6	847	1	CD22_HUMAN
23	211	9.6	4391	1	PGBM_HUMAN
24	209.5	9.5	345	1	OPCM_RAT
25	209	9.5	353	1	CEPU_CHICK
26	207.5	9.4	509	1	SHS1_RAT
27	207.5	9.4	646	1	MUS1_HUMAN
28	207	9.4	1493	1	NEO1_MOUSE
29	206.5	9.4	338	1	LAMP_HUMAN
30	206.5	9.4	862	1	CD22_MOUSE
31	204.5	9.3	338	1	LAMP_RAT
32	204	9.3	702	1	CEAS_HUMAN
33	203.5	9.3	583	1	C166_HUMAN

34	203	9.2	1461	1	NEO1_HUMAN	Q92859 homo sapien
35	202	9.2	1443	1	NEO1_CHICK	Q90610 gallus gall
36	198	9.0	1377	1	NEO1_RAT	P97603 rattus norv
37	197	9.0	3707	1	PGBM_MOUSE	Q05793 mus musculu
38	196.5	8.9	1241	1	NPHN_HUMAN	Q05000 homo sapien
39	196.5	8.9	1331	1	CTA2_HUMAN	Q09066 homo sapien
40	195	8.9	506	1	SHS1_BOVIN	O46631 bos taurus
41	194	8.8	1091	1	NCA1_CHICK	P13590 gallus gall
42	193	8.8	761	1	NCA2_HUMAN	P13592 homo sapien
43	192.5	8.8	848	1	NCA1_HUMAN	P13591 homo sapien
44	192.5	8.8	1036	1	AXO1_CHICK	P28685 gallus gall
45	191.5	8.7	853	1	NCA1_BOVIN	P31836 bos taurus

ALIGNMENTS

RESULT 1	ID	Accession	Standard	PRT	515 AA.
PVR1_PIG	AC	Q9G176			
16-OCT-2001 (Rel. 40, Last sequence update)	DT	16-OCT-2001 (Rel. 40, Last sequence update)			
10-OCT-2003 (Rel. 42, Last annotation update)	DT	10-OCT-2003 (Rel. 42, Last annotation update)			
Poliiovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (HVEC) (Nectin 1).	DE	PVR1L OR PVR1 OR HVEC.			
Sus scrofa (Pig).	OS	Sus scrofa (Pig).			
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.	OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
NBI_TaxId=9823;	OX	NBI_TaxId=9823;			
SEQUENCE FROM N.A.	RX	MEDLINE=21176378; PubMed=11277703;			
Malne R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J., Cohen G.H.,	RA				
"Porcine HVEC, a member of the highly conserved HVEC/nectin 1 family, is a functional alphaherpesvirus receptor."	RT				
Virology 281:315-328(2001).	RL				
-1- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR ALPHABERPEVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO CELLS.	CC				
-1- SUBUNIT: Interacts with HSV glycoprotein D (gD) (By similarity).	CC				
-1- SUBCELLULAR LOCATION: Type I membrane protein.	CC				
-1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.	CC				
-1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.	CC				

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EMBL; AF308632; AAC30281.1; -	DR				
HSSP; P06907; INET.	DR				
InterPro; IPR007110; IG-like.	DR				
InterPro; IPR003596; IG_V.	DR				
Pfam; PF00047; Ig_2.	DR				
SMART; SM00406; IGV_1.	DR				
PROSITE; PS50835; IG-LIKE; 2.	KW				
Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane; Repeat; Glycoprotein; Signal.	KW				
SIGNAL	FT				
CHAIN	FT				
DOMAIN	FT				
TRANSMEM	FT				
DOMAIN	FT				
DOMAIN	FT				
DOMAIN	FT				
DOMAIN	FT				
DOMAIN	FT				
DOMAIN	FT				
POLY-GLU.	FT				

FT DOMAIN 444 447 POLY-GLY.
 FT DISULFID 51 124 BY SIMILARITY.
 FT DISULFID 172 226 BY SIMILARITY.
 FT DISULFID 269 316 BY SIMILARITY.
 FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 286 286 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 307 307 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 515 AA; 57047 MW; BFAB00320DEB3785 CRC64;

Query Match 11.8%; Score 259.5; DB 1; Length 515;
 Best Local Similarity 24.5%; Pred. No. 2.2e-11;
 Matches 107; Conservative 61; Mismatches 165; Indels 103; Gaps 18;

QY 34 VVYIEGSEVATISGVKSDSVIQLNPNKQITVFRDFPLKDSFQLNFSSEELKVL 93
 DB 62 ITQVYWKATNGSKON-----VAINPANGVSLAPYR-----ERVEPLRPSTDOTIRL 111
 QY 94 TNVSIIDEGRYFCQLYTDP--QESYTTITVLPSPNLMIDQ-----KDTAVEGEE 143
 DB 112 SRLIEDEGVYICEFATFPAGNRESQNLITVMKPTNWIEGTQAVLRKKKDDKV---- 167
 QY 144 IEVNTCTMAKSPATITRMFKNKEIKGKSEVEEM---SDVYVTSQMLKVKHEDGVYV 200
 DB 168 LVATCTBANGKBPVSWM---ETHLKGAEVYQIRPNNGVYISRYLRVPSREDRQSL 224
 QY 201 ICQVHEPAVNTGNLTQRY-----LEVQYKPOVHIQ--MTYPLQGLTREGDAFELTCEAI 252
 DB 225 ACIV-----NHYMDFRESLTNVQYEPVTEIGDGMWYLQRM-----VKLTCKAD 272
 QY 253 GKPOPVVTVYRVDDEPQNAVLSGPNLPTNN-LNKTDNCTYCEASNIVGKASHSNLY 311
 DB 273 ANPFAPEYHWTTLNGSLPKGVKQVGNRLTFRGPTNYSMACTYCEANPTGTRSGOVEN 332
 QY 312 VYDPTTIPPTTTTITTTTITTTTITTTITTTITTTITTTITTTITTTITTTITTTITTT 367
 DB 333 ITEPPTPSP-----HGRAGVGPVTAIGGVGSLVLV 368
 QY 368 PAMLCILITIGRYARKHGYFT-----HEAKGA-----DMAADADR 405
 DB 369 FVVGIGIVVLCRRHTEKGYSTKSHVYNGYSKAGIPQHPMPAONLQYVEDSDDEKKA 428
 QY 406 IINAGGONNSEKKE 421
 DB 429 --GPLGGSSYESEEE 442

RESULT 2

PRI1 HUMAN STANDARD; PRT; 517 AA.
 AC Q15223; Q15223; Q15223; Q15223; Q15223; Q15223; Q15223; Q15223; Q15223; Q15223;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Poliovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (Hvrc) (Nectin 1) (Herpesvirus Ig-like receptor) (HIGR) (CD111 antigen).
 GN PVR1 OR PVR1 OR HVRC.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM DELTA).
 RX MEDLINE=95237621; PubMed=7721102;
 RA Lopez M., Eberle F., Mactel M.-G., Gabert J., Bardin F., Marc C., Dubreuil P.;
 RT "cDNA characterization and chromosomal localization of a gene related to the poliovirus receptor gene";

RL Gene 155:261-265 (1995).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM DELTA).
 RX MEDLINE=98279152; PubMed=9616127;
 RA Geraghty R.J., Krummenacher G., Cohen G.H., Eisenberg R.J., Spear P.G.;
 RT "Entry of alphaherpesviruses mediated by poliovirus receptor-related protein 1 and poliovirus receptor";
 RL Science 280:1618-1620 (1998).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM GAMMA).
 RX MEDLINE=21256041; PubMed=11356977;
 RA Lopez M., Cocchi F., Avitabile B., Leclerc A., Adelaide J., Camdepoli F., Dubreuil P.;
 RT "Novel, soluble isoform of the herpes simplex virus (HSV) receptor nectin (or pvr1-Hvrc) modulates positively and negatively susceptibility to HSV infection";
 RT J. Virol. 75:5684-5691 (2001).
 RN [4]
 RP SEQUENCE OF 28-517 FROM N.A. (ISOFORMS ALPHA AND DELTA), AND DISEASE. MEDLINE=20392396; PubMed=10932188;
 RX Suzuki K., Hu D., Bustos T., Zlotogora J., Richieri-Costa A., Helms J.A., Spritz R.A.;
 RA "Mutations of PVR1, encoding a cell-cell adhesion molecule/herpesvirus receptor, in cleft lip/palate-ectodermal dysplasia";
 RT Nat. Genet. 25:427-430 (2000).
 RL "FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO CELLS."
 CC - SUBUNIT: Interacts with HSV glycoprotein D (gD).
 CC - SUBCELLULAR LOCATION: Type I membrane protein (isoforms alpha and delta). Secreted (isoform gamma).
 CC - ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=Delta;
 CC IsoId=Q15223-1; Sequence=D:displayed;
 CC Name=Alpha;
 CC IsoId=Q15223-2; Sequence=VSP_002626, VSP_002627;
 CC Name=Gamma;
 CC IsoId=Q15223-3; Sequence=VSP_002624, VSP_002625;
 CC - DISEASE: Defects in PVR1 are a cause of cleft lip/palate-ectodermal dysplasia syndrome (CLPED1) [MIM:225000]. CLPED1 is responsible for allelic forms known as Margarita island ectodermal dysplasia [MIM:225060] and Zlotogora-Oguz syndrome.
 CC - SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC - DATABASE: NAME=PROV; NOTE=PROV 2:45-49 (2001);
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/guide/2005693930_g.htm".
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 CC
 CC EMBL: X76400; CAA53980.2; ALT_INIT.
 CC EMBL: AF060231; AAC23798.1; -
 CC EMBL: AY029539; AAK3124.1; -
 CC EMBL: AF252867; AAG16648.1; -
 CC EMBL: AF196768; AAG16648.1; JOINED.
 CC EMBL: AF196769; AAG16648.1; JOINED.
 CC EMBL: AF196770; AAG16648.1; JOINED.
 CC EMBL: AF196771; AAG16648.1; JOINED.
 CC EMBL: AF196774; AAG16649.1; -
 CC EMBL: AF196768; AAG16649.1; JOINED.
 CC EMBL: AF196769; AAG16649.1; JOINED.
 CC EMBL: AF196770; AAG16649.1; JOINED.
 CC EMBL: AF196771; AAG16649.1; JOINED.
 CC EMBL: AF196772; AAG16649.1; JOINED.
 CC EMBL: AF196773; AAG16649.1; JOINED.

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DR Genew; HGNC:9706; PVR1.
DR MIM; 60644; -.
DR MIM; 22500; -.
DR MIM; 22506; -.
DR GO; GO:0016021; C.integral to membrane; NAS.
DR GO; GO:004895; F.cell adhesion receptor activity; NAS.
DR GO; GO:0015028; F.coreceptor activity; NAS.
DR GO; GO:0006955; P.immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane;
KW Repeat; Glycoprotein; Signal; Alternative splicing.
FT SIGNAL 1 30
FT CHAIN 31 517
FT DOMAIN 31 355
FT TRANSMEM 356 376
FT DOMAIN 377 517
FT DOMAIN 31 141
FT DOMAIN 149 238
FT DOMAIN 247 334
FT DOMAIN 437 444
FT DISULFID 51 124
FT DISULFID 172 226
FT DISULFID 269 316
FT CARBOHYD 36 72
FT CARBOHYD 72 139
FT CARBOHYD 139 202
FT CARBOHYD 202 286
FT CARBOHYD 297 307
FT CARBOHYD 307 332
FT CARBOHYD 332 352
FT VASPLIC 353 517
FT VASPLIC 336 458
FT VASPLIC 459 517
FT VASPLIC 517 517
FT SEQUENCE 517 AA; 57158 MW; DF34C8AE8C93EE6D CRC64;
Query Match 11.5%; Score 252.5; DB 1; Length 517;
Best Local Similarity 25.2%; Pred. No. 7e-11;
Matches 104; Conservative 59; Mismatches 155; Indels 95; Gaps 19;
QY 56 IQLNPNRQITVYFDFRPLKDSRFOLNFSSELSKSTVNVISIDEGRYCOLATDP-- 113
DB 78 VAINPMSGVSVLAPYR---ERVEFLRPSTDTGTLISRLIEDDEGVYICERPTPTGN 133
QY 114 QESTTTTIVLPNNLMIDICKD-TAVGESEIEV--NCTAMASKPATTRMEKGNELK 169
DB 134 RESQINLVAKPTNWTIEGTQAVLRKKQGDKVLVATCSANGKPPSVSM--ETRLK 190
QY 170 GKSEVEEM---SDMYTYSOLMLKVHKEDGVPIQGVHRAVYNGIQOTRY-----LEY 221
DB 191 GEAYQVIRNNGVYVTSRVLVPSRAHQSIACIV-----NTHMDFKESLTINV 243
QY 222 QYKQVHIQ---MTYPIQGLTRFEDAFELTGEATIGKQPVWTVVVRVDDMPQHAVLSGP 278
DB 244 QYEEVLTIEGFDGMVYIQMD-----VLTICKADANPAPNHYHTTLNGLSPKGVENQR 298

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QY 279 NLFINN-LAKTNGTYRCEASNIYGRKADSYMLVYDPTTTPPTTTTTTTTTTIL 337
DB 299 TLFFKGINVSLAGTYICETNPISGRSGVEVNTPEFTPTSP----- 343
QY 338 TIITDSRAGEEG-TIGAVDHAIVGVAVVVFAMLCILIIIGRYFA----RH--KGYFT 390
DB 344 -----EHGRAGVPTPAIIGVAGSI---LVLIVGVIGIVALLRRRRHFKGDYST 391
QY 391 -----HEAKGA-----DDAADADTAIINABGCONNSEKKE 421
DB 392 KKAHYNGYSKAGIPQHHPMAQNLQYPPDSDEKKA--GPIGSSSYEEEEE 442
RESULT 3
PVR2 MOUSE STANDARD; PRT; 530 AA.
ID PVR2 MOUSE
AC P32507; 062096;
DT 01-OCT-1993 (Rel. 27, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Poliovirus receptor related protein 2 precursor (Murine herpesvirus
DE entry protein B) (MHV8B) (Nectin 2) (Poliovirus receptor homolog).
GN PVR12 OR PVS OR PVR OR MPH.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=92219365; PubMed=1560525;
RA Morrison M.E., Racanelli V.R.;
RT "Molecular cloning and expression of a murine homolog of the human
RL poliovirus receptor gene.";
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM BETA).
RX STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=94179228; PubMed=8132569;
RA Aoki J., Koike S., Ise I., Sato-Yoshida Y., Nomoto A.;
RT "Amino acid residues on human poliovirus receptor involved in
RT interaction with poliovirus.";
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM BETA).
RX STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.U., Ustin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millhys S.J.,
RA Bosak S.A., McMan P.C., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Vallilon D.K., Muzny D.M., Sodergren E.U., Lu X., Gibbs R.A.,
RA Rahy J., Helton E., Kettlemen M., Madan A.C., Rodchik S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shachenko Y., Bouffard G.G.,
RA Blakesley R.W., Tuchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherach A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=99214397; PubMed=10196354;
RA Shukla D., Rowe C.L., Dong Y., Racanelli V.R., Spear P.G.;
RT "The murine homolog (Mpr) of human herpesvirus entry protein B (HvB)
RT mediates entry of pseudorabies virus but not herpes simplex virus
RT types 1 and 2.";

```

Qy	100	DEGGYFCQLYTDP--PQESTYTTTTLVLPKPNIMIDICKDPAVGEELV-----NCT	143
Db	125	DEGNYTCEPAPTEPFGTGRGVTWLRVLIQAPEN-----HAKEQVTLIPQSVAVARCV	175
Qy	150	AMASKPATTIRWFG-NKEIKGSEVSEWSDMTVTSQLMKVAKEDGCVPLICQVEHPA	208
Db	176	STGGRPPARLTITWISSLGGKAKDIOEPDIOAGTYIIIRSYSLVPPGRADGVKVTGRVHES	235
Qy	209	VTGNLQOTORYLEVQYKQPOVHIQMTYPLQGLTRGDAFELTCEALIGKQPPWATTVRVDD	268
Db	236	FEEDILPVLITSLVRYPEVEIS-GYDNNWYLGSESAI-LTCDVRSNPEPDYDSTTSGV	293
Qy	269	MPQNAVLSGNPLFINLNKTDNGYTRCEASINVKASDMLYYDDPTTIPETTTT	328
Db	294	FPASAVAGSQQLVHSDVRKWNTEFCTANAVGTGSAEOVILVRESPT-----	343
Qy	329	TTTTTTTLITITDSRAGEEGTIGAVDHAVIGVAVV	367
Db	344	-----AGAGATGG-----IIGGIAMAI	361

RESULT 4			
SVR2_HUMAN	STANDARD;	PRF;	538 AA.
AC	Q92692: 075455: 096429:		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DE	Poliiovirus receptor related protein 2 precursor (Herpes virus entry mediator PR2 (HvEB) (Nectin 2) (CD112 antigen)).		
DE	PVR2 OR PR2 OR HVEB.		
OC	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
UN	[1]		
RP	SEQUENCE FROM N.A. (ISOFORM DELTA).		
RX	MEDLINE=95347610; PubMed=7622062;		
RA	Eberle F., Dubreuil P., Mattei M.-G., Devilard E., Lopez M.,		
RT	"The human PRR2 gene, related to the human poliovirus receptor gene		
RL	(PVR), is the true homolog of the murine MPN gene.";		
RL	Gene 159:267-272(1995).		
UN	[2]		
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).		
RX	MEDLINE=98321161; PubMed=9657005;		
RA	Warner M.S., Geraghty R.J., Martinez W.M., Montgomery R.I.,		
RA	Whitbeck J.C., Xu R., Eisenberg R.U., Chen G.H., Spar P.G.,		
RT	"A cell surface protein with herpesvirus entry activity (HvEB) confers		
RT	susceptibility to infection by mutants of herpes simplex virus type		
RL	1, herpes simplex virus type 2, and pseudorabies virus.";		
RL	Virology 246:179-189(1998).		
UN	[3]		
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).		
RX	TISUS=Brain;		
RC	MEDLINE=22388257; PubMed=12477932;		
RA	Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,		
RA	Altshul S.F., Zeeberg B., Butler K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diachenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schetz T.E.,		
RA	Brownstein M.U., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.U.,		
RA	Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,		
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahy U., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whitesley M., Madan A., Young A.C., Shevchenko Y., Bouford G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,		
RA	Buterfiguez Y.S.N., Krzyzinski M.I., Skalska U., Smalhus D.E.,		
RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;		

FT	CARBOHYD	137	137	N-LINKED (GLCNAC...)	(POTENTIAL).
FT	CARBOHYD	324	324	N-LINKED (GLCNAC...)	(POTENTIAL).
FT	VARSPLIC	351	479	NTAAGATGATGGTGGTAATAATTAAATGATGILCROQRKQCTL	.GAEBDEDLBGPSTPTPRAKLEAOEMPSQLFTLGASEH SPLKTTPYFDAGASCTGEOMPRYNHELPTLEERSGAPHPATS LGSPIP -> RASPRDVGPLWVGAGVTLVLLLAGASTLA FILTRVRARRSGPGAGGADGGVFDPKPQVLGNQGVF MTPVVGGPMERBDGDDEEEREERKEKELMPPPALDDDM ESOLDGSLISRRAYVV (in isoform Alpha).
FT	VARSPLIC	480	538	/FTid=VSP_002628.	Missing (in isoform Alpha).
FT	SEQUENCE	538 AA;	57742 MW;	3AE4FE3BE92FEF624 CRC64;	
SQ	Query Match	Best Local Similarity	10.9%;	Score 238.5;	DB 1; Length 538;
	Matches 110;	Conservative 63;	Mismatches 196;	Indels 113;	Gaps 17;
OY	2	APGRLRLLLLLLSAALLPTDGQMLFTDXVTVIEBEAVATISCQVKNKSDSVIOLNRP	61		
Db	12	SPRPLFLMPILLLL-----LLETG-AQDVRAQVULREVRG-----QLGGTVELPCHLRP	59		
OY	62	-----NRQTIFRDRPLKLDSRF-----QLNNSSG-----	87		
Db	60	VPGLYISLVTWORPDAPANHQN--AAFHPKMGPSFPSPKGSERLSFSVASKOSTGODTE	117		
OY	88	----ELKXSLTNVISIDEGRYFCQLYDPR--PSESYYTIITVLPVRNMIDIOKDVAEG	141		
Db	118	AELQDATLALHGLVEDEGNATCEPAITFPKKSVMGMWLRIYARKN-QALAOKTTPESD	176		
OY	142	EELVENCTAMASKAATITTFMKG-NKELKGSEYEWSDMYTTSQLMKVNKEDDGYV	200		
Db	177	PTVALCISKRGEPARIISMUSLSDMEAKERQVSGTLAIVTIVSRFLVPSGRADGYTV	236		
OY	201	ICQVEHAVMGNLTQORYLEVQYKRYOHNITMYLQGITREGDAFELLCEALIGKOPRMV	260		
Db	237	TCKTEHSFEPRALIPTLSIKRYPEVIS-GYDDNMYLGRTD-TSCDVRSNDEPTY	294		
OY	261	TWEVDDEMPHOAVLAGEPNLFINNLTNDNGTYRCASNIVGKAHSDMYLYVDEPTTIP	320		
Db	295	DMSITSGTFPSAVAQSQSLVIHAVDSLFTMTFVCVTNNAWGMRAGVILVEREPTNT--	352		
OY	321	PRTTTTTTTTTTTTTLITLITDSAGSEGITGADVAVIGVVAVVVFAMCLLIIGRY	380		
Db	353	-----AGAGATGG-----IIIGLIAIAITAATAATGILCR	383		
OY	381	FARHGTYFTHBAKADDAAD-----TAINAE-----GGONNSEKK	421		
Db	384	QQREQR-----LQGAEBDEDLBGPSTPTPRAKLEAOEMPSQLFTLGASEHSPKTP	438		
OY	422	YF 423			
Db	439	YF 440			

RESULT 5

PVR_CERAE	STANDARD;	PRT;	417 AA.
AC P32506;			
DT 01-OCT-1993 (Rel. 27, Created)			
DT 01-OCT-1993 (Rel. 27, Last sequence update)			
DT 10-OCT-2003 (Rel. 42, last annotation update)			
DE Poliovirus receptor precursor.			
OS PVR OR PVS.			
OC Cercopithecus aethiops (Green monkey) (Grivet).			
OC Eukaryota; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Theria; Primates; Catarrhini; Cercopithecoidea;			
OC Cercopithecinae; Cercopithecus.			
NCBI_TaxID=9534;			
RN [1]			
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND DELTA).			
RC TISSUE=Kidney;			
RX MEDLINE=93059651; PubMed=1331508;			

OY	57	QLNLNPR-----QTVIRDRDRPLKDSFOLLNNESSSELKXSLTNVS-----ISDEGRY	104
Ds	62	SQLTWSHGSGSMANVHQTQCPNYSPEPKLEFVAALGVELLDASLRMGRLNREDEGNY	121
OY	105	FCQLYTDPDPQESYTT---ITLVEPPRNLMIDIQKDAVEGESELEV-NCITAMASKPATITR	160
Ds	122	TC-LFVTFPGSSSVDILRLVLAKPQV-TAEVCK-VQLTKKPPVAVRCVSGRPPAHIT	178
OY	161	WPKNKEKLKKESEVEE-----WSDMYTTSQMLMKVHEDDGVPVPCGVHEPAVYGNLQTO	216
Ds	179	W-HSULGGMPTNSQAPGLSGTIVTSLMILVPSQVDGKSTCKVHEHSEFPKPOLLT	235
OY	217	RYLEVOYKPPVQHIQMTYPTLOGLTREEDGPAFELTCEAIKQPPVMVTVWRVVDENDQHAVLS	276
Ds	236	VNLTVYYPEPVVIS-GYDNNWYLSQNEA-LTTCGASNPBPTGYNWTMGPLDPFAVAQ	293
OY	277	GENPFINNLKNTDNGYTRCEASNVVGAHSDYMLYVDPPTTIPPTTTTTTTTTTTT	336
Ds	294	GAQQLILIPVVKPIITTFICNVYALGARGQAELEVTVQVEKGPSEPS-----	338
OY	337	LTITDSRAGEBGTIGADVHVGVAVVFAMCLILILGRYFAHKGH---YFTHE	392
Ds	339	-----GSSNITIIILLIGIVL---LTLLLGIVGYFYHRSRGRBFLMCHHL	380
OY	393	AKGADDAADADTALINAECCNNSEKKE	421
Ds	381	SPSSEHNSA-----SANGYISYSDVSR	404

RESULT 6

PVRI	MOUSE	STANDARD;	PRT;	515	AA.
ID	PVRI	MOUSE			
AC	Q9UKF6;	Q9ERL5;	Q9Q117;		
DT	16-OCT-2001	(Rel. 40,	Created)		
DT	16-OCT-2001	(Rel. 40,	Last sequence update)		
DT	15-MAR-2004	(Rel. 43,	Last annotation update)		
DE	Poliiovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (HvEC) (Nectin 1).				
DE	PVRI1 OR PRR1 OR HVEC.				
GN	Mus musculus (Mouse).				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
CX	NCBI_TaxId=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=20243787; PubMed=10781093;				
RA	Menotti L., Lopez M., Avitabile E., Stefan A., Cocchi F., Adelaide J.,				
RA	Lecocq E., Dubreuil P., Campadelli-Fume G.;				
RT	"The murine homolog of human nectin delta serves as a species				
RT	nonspecific mediator for entry of human and animal alpha herpesviruses				
RT	in a pathway independent of detectable binding to gD.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 97:4867-4872(2000).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=20541977; PubMed=11090177;				
RA	Shukla D., Dal Canto M.C., Rowe C.L., Spear P.G.;				
RT	"Striking similarity of murine nectin-1alpha to human nectin-1alpha				
RT	(HvEC) in sequence and activity as a glycoprotein D receptor for				
RT	alphaherpesvirus entry.";				
RL	J. Virol. 74:11773-11781(2000).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Swiss Webster;				
RA	Zhan J., Wimmer E.;				
RT	"Mouse nectin-1 (mPRR1), a herpesvirus receptor, is expressed in the				
RT	floor plate during embryogenesis, suggesting a role in neural				
RT	development.";				
CC	Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.				
CC	-1- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR				
CC	ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO				
CC	CELLS.				
CC	-1- SUBUNIT: Interacts with HSV glycoprotein D (gD).				
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.				


```

CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -----
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CC -----
DR EMBL; AF239762; AAF60333.1; -
DR EMBL; AF270977; AAF6195.1; -
DR EMBL; AF297665; AAG22808.1; -
DR MGI; MGI:1926483; PVT11.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0004872; F:receptor activity; IDA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003599; IG.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00409; Ig_2.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane;
KW Repeat; Glycoprotein; Signal.
FT SIGNAL 1 30
FT CHAIN 1 30
FT DOMAIN 31 515
FT TRANSMEM 31 354
FT TRANSMEM 355 375
FT DOMAIN 376 515
FT DOMAIN 31 141
FT DOMAIN 145 243
FT DOMAIN 247 334
FT DOMAIN 436 442
FT DOMAIN 443 447
FT DISULFID 51 124
FT DISULFID 172 226
FT CARBOHYD 269 316
FT CARBOHYD 36 36
FT CARBOHYD 72 72
FT CARBOHYD 139 139
FT CARBOHYD 202 202
FT CARBOHYD 286 286
FT CARBOHYD 297 297
FT CARBOHYD 332 332
FT CONFLICT 138 138
FT CONFLICT 165 165
FT CONFLICT 342 342
FT CONFLICT 428 428
SQ SEQUENCE 515 AA; 57064 MW; FFF608B5FFB7A0F CRC64;

Query Match 10.7%; Score 236; DB 1; Length 515;
Best Local Similarity 24.9%; Pred. No. 1,1e-09;
Matches 99; Conservative 59; Mismatches 144; Indels 96; Gaps 19;

73 PLKSRQQLANTSSSELSKSLTNSISDEGRFCQLYTDP--QESYTTITVLPPTNIM 130
91 PPYKRVFELRPSTIDGIRLSGLEDEGNYICEFATPTGRRSGLNTVWAKPLTW- 149
131 IDIKQVAV---EGEIEV---NCTAMASKPATITIMFGNKELKSKSVSEW---SDM 180
150 --LEGTAAVLRARGQGNKLVATCTISANGKPSBAVW---ETRLKSEAIVQIIRNPNGT 204
181 YTTVSQMLKVKHKEDGVPIVCOYEHPAVTGNLTQORY-----LEVQKPOVAHQMTYLP 235
205 VTVISRYLVPSRAHROSACIV-----NYILDFRESLITLVQYESEVTI----- 251
236 OGTLREEDAF-----ELTCEALGKQPPVWVWTVRVVDENRQAVISGRPLFIN-LINK 288
252 EGF--DQWYTIQRTDVLTCTKADANPATEYHMTLNGSLPKQVEAKNRTLFRGPTYS 309
289 DNGTYRCEASNIIVGKASHDVMLVYDPPPTITPTTTTTTTTTTTTTTTTTLITLIDSPRAGE 348

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DB 310 LACTYCEANTNPIGRSQGVENVTEFPYT-PTPE-----HGRRAGOM 351
CY 349 GTIGAVDHAIVIGQVAVVFAFMCC--LLIILGRYFAHKGYFT----- 390
DB 352 PT-----AIIQVAGSVLLVLIIVGGITVALRRRRHTKGDYSTKHYGVNGYSKAGLP 405
CY 391 -HEAKGA-----DDAADADTAIIINAEQGNNSKEKE 421
DB 406 QHHPMAQNIQYBDDSDDEKKA--SPLGGSSYESEEE 441

RESULT 7
NCBI_XENIA STANDARD; PRT; 1088 AA.
ID NCBI_XENIA
AC P16170;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Neural cell adhesion molecule 1, 180 kDa isoform precursor (N-CAM
DE 180).
GN NCAM1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS N-CAM 140 AND N-CAM 180).
RX MEDLINE=90098871; PubMed=2481269;
RA Krieg P.A., Sakaguchi D.S., Kintner C.R.;
RT "Primary structure and developmental expression of a large
RT cytoplasmic domain form of Xenopus laevis neural cell adhesion
RT molecule (NCAM).";
RL Nucleic Acids Res. 17:10321-10335(1989).
CC -1- FUNCTION: This protein is a cell adhesion molecule involved in
CC neuron-neuron adhesion, neurite fasciculation, outgrowth of
CC neurites, etc.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Name=N-CAM 180;
CC IsoId=P16170-1; Sequence=Displayed;
CC Name=N-CAM 140;
CC IsoId=P16170-2; Sequence=VSP_002589;
CC -1- TISSUE SPECIFICITY: Expressed in neuron and in presumptive neural
CC tissue.
CC -1- DEVELOPMENTAL STAGE: THE MNA ENCODING THIS LD-NCAM IS THE MAJOR
CC TRANSCRIPT PRESENT IN BOTH MATERNAL RNA AND IN THE EMBRYO DURING
CC EARLY NEURAL DEVELOPMENT.
CC -1- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M25696; AAA49909.1; -
DR PIR; S09600; IXXLNL.
DR HSSP; P56276; ITLK.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_C2.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; Ig_5.
DR SMART; SM00408; FN3; 2.
DR SMART; SM00406; IG2; 5.
DR PROSITE; PS50835; IG_LIKE; 5.
KW Cell adhesion; Glycoprotein; Transmembrane; Repeat;

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[illegible]


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FT      CONFLICT      75      75      (Potential).
FT      CONFLICT      92      S -> G (IN REF. 1).
FT      CONFLICT      119     T -> I (IN REF. 1).
FT      CONFLICT      187     E -> Q (IN REF. 1).
FT      CONFLICT      213     R -> P (IN REF. 1).
FT      CONFLICT      225     I -> F (IN REF. 1).
SQ      SEQUENCE      344 AA; 37984 MW; C885B8A52C148554 CEC64;

Query Match      10.6%; Score 232; DB 1; Length 344;
Best Local Similarity 26.2%; Pred. No. 1.3e-09;
Matches 85; Conservative 57; Mismatches 133; Indels 50; Gaps 15;

QY      10 LLLLLLAAALIPFG---DQGNLFK---DYVIEGAVATSCQVNSKDSVYQLNPN 62
DB      14 LVVSLRLFLFVPTGVPRSGDAFPKAMDVTVVAGSASATLRCTI---DKRVTVVWLN 70
QY      63 RQTI-YFRDPRPLKDSRFQNLNFSSELKSLTNVSISSDEGRYFQGLYTD--PROESYTTI 120
DB      71 RSTIIYAGNDKMKCDLPRVVLSTNQTQYSIEIQNVVDDEGPTCSVTDNHPKTSRVHL 130
QY      121 TVLVPNNMLTIDIQDQAV--EGEIEVNCCTAMASKPATITMFKGNKELKGSSEVMSD 179
DB      131 IVQVSPK--IVEISSDISINEGNNSITLCTIA-TGRPEPTVWRIHSPKAVGVSEDEYLE 187
QY      180 MYVTLSQMLMKVH---KEDDGVPIQVYEHFPAVNGNLQTVYLVQVYKQVHIGMTYPLQ 236
DB      188 IQGITRESGGEYECASNDVAAPVRRVK-----VTNVPYYS---EAK 229
QY      237 GL-TREGDAFELTCEAIKPOFVMTVTVVVDDEMPQ-----HATVSGNLFNNLN 286
DB      230 GTGVGVGQKGLQCEASAVPS-ABEQWFKDKRLVEGKKGVKVENRPLSLTLTF--NVS 286
QY      287 KTDNCTYCEASNTYGAHSDYMLY 311
DB      287 EHDYGNVTCVASNKLGHNTASIMLF 311

RESULT 9
PVR_HUMAN
ID      PVR_HUMAN      STANDARD.      PRT;      417 AA.
AC      P15151; P15152; Q15267; Q15268;
DT      01-APR-1990 (Rel. 14, Created)
DI      01-FEB-1996 (Rel. 33, Last sequence update)
DR      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Poliovirus receptor precursor (CD155 antigen).
GN      PVR OR PVS.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A. PubMed=253845;
RX      Mendelsohn C.L., Wimmer E., Racanelli V.R.;
RA      "Cellular receptor for poliovirus: molecular cloning, nucleotide
RT      sequence, and expression of a new member of the immunoglobulin
RT      superfamily."
RL      Cell 56:855-865 (1989).
RN      [2]
RP      REVISIONS.
RA      Racanelli V.R.;
RL      Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX      MEDLINE=9106015; PubMed=2170108;
RA      Koike S., Horie H., Ise I., Okitsu A., Yoshida M., Iizuka N.,
RT      Takeuchi K., Takegami T., Nomoto A.;
RT      "The poliovirus receptor protein is produced both as membrane-bound
RL      and secreted forms."
RN      [4]
RP      EMBL J. 9:3217-3224 (1990).
RP      SEQUENCE FROM N.A.

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RA      Kodoyianni V., Severin J., Ge Y., Grable J., Kvistad E., Gordon J.,
RA      Shannon M., Brower A., Olsen A.S., Smith L.M.;
RT      "Sequence analysis of a 1Mb region in 19q13.2 containing a zinc finger
RT      gene cluster."
RL      Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN      [5]
RP      DOMAINS.
RX      MEDLINE=91239515; PubMed=1851992;
RA      Koike S., Ise I., Nomoto A.;
RT      "Functional domains of the poliovirus receptor";
RL      Proc. Natl. Acad. Sci. U.S.A. 88:4104-4108 (1991).
RN      [6]
RP      MUTAGENESIS OF CARBOHYDRATE-LINKAGE SITES.
RX      MEDLINE=93059689; PubMed=1331527;
RA      Zibert A., Wimmer E.;
RT      "N-glycosylation of the virus binding domain is not essential for
RT      function of the human poliovirus receptor."
RL      J. Virol. 66:7368-7373 (1992).
CC      -1- FUNCTION: Not known. Used by poliovirus to bind and enter the
CC      cell.
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms alpha and
CC      delta). Secreted (isoforms beta and gamma).
CC      -1- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=4;
CC      Name=Alpha;
CC      IsoId=P15151-1; Sequence=Displayed;
CC      Name=Beta;
CC      IsoId=P15151-2; Sequence=VSP_002617;
CC      Name=Gamma;
CC      IsoId=P15151-3; Sequence=VSP_002618; VSP_002619;
CC      Name=Delta;
CC      IsoId=P15151-4; Sequence=VSP_002620; VSP_002621;
CC      -1- MISCELLANEOUS: THE V-TYPE DOMAIN IS NECESSARY AND SUFFICIENT FOR
CC      VIRUS BINDING AND UPTAKE.
CC      -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC      -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC      -1- DATABASES: NAME=PROV; NOTE=CD guide CD155 entry;
CC      WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd155.htm".
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; M24407; AAA36461.1; -
DR      EMBL; M24406; AAA36462.1; -
DR      EMBL; X64116; CAA45478.1; -
DR      EMBL; X64117; CAA45478.1; JOINED
DR      EMBL; X64118; CAA45478.1; JOINED
DR      EMBL; X64119; CAA45478.1; JOINED
DR      EMBL; X64120; CAA45478.1; JOINED
DR      EMBL; X64121; CAA45478.1; JOINED
DR      EMBL; X64122; CAA45478.1; JOINED
DR      EMBL; X64123; CAA45478.1; JOINED
DR      EMBL; X64116; CAA45479.1; -
DR      EMBL; X64117; CAA45479.1; JOINED
DR      EMBL; X64118; CAA45479.1; JOINED
DR      EMBL; X64119; CAA45479.1; JOINED
DR      EMBL; X64120; CAA45479.1; JOINED
DR      EMBL; X64121; CAA45479.1; JOINED
DR      EMBL; X64122; CAA45479.1; JOINED
DR      EMBL; X64123; CAA45479.1; JOINED
DR      EMBL; X64116; CAA45480.1; -
DR      EMBL; X64117; CAA45480.1; JOINED
DR      EMBL; X64118; CAA45480.1; JOINED
DR      EMBL; X64119; CAA45480.1; JOINED
DR      EMBL; X64120; CAA45480.1; JOINED
DR      EMBL; X64121; CAA45480.1; JOINED
DR      EMBL; X64122; CAA45480.1; JOINED
DR      EMBL; X64123; CAA45480.1; JOINED
DR      EMBL; AC069848; AAF69803.1; -

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DR PIR; A43024; RMHUPD.
DR PIR; S12048; RMHUPA.
DR Genew; HGNC:9705; PVR.
DR MIM; 173850; -.
DR GO; GO:0005737; C:cytoplasm; TAS.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0007125; P:invasive growth; TAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00406; IgV_1.
DR PROSITE; PS50835; IG_Like; 3.
KW Immunoglobulin domain; Receptor; Polymorphism.
KW Repeat; Antigen; Alternative splicing; Polymorphism.
FT SIGNAL 1 20
FT CHAIN 21 417
FT DOMAIN 21 343
FT TRANSMEM 344 367
FT DOMAIN 368 417
FT DOMAIN 24 139
FT DOMAIN 145 237
FT DOMAIN 244 328
FT DISULFID 49 123
FT DISULFID 166 221
FT DISULFID 266 312
FT CARBOHYD 105 105
FT CARBOHYD 120 120
FT CARBOHYD 188 188
FT CARBOHYD 218 218
FT CARBOHYD 237 237
FT CARBOHYD 278 278
FT CARBOHYD 307 307
FT CARBOHYD 313 313
FT VASPLIC 340 384
FT VASPLIC 331 331
FT VASPLIC 332 384
FT VASPLIC 385 392
FT VASPLIC 393 417
FT VASPLIC 67 67
FT VARIANT 340 340
FT SEQUENCE 417 AA; 45302 MW; DISC012CE85169B CRC64;

Query Match 10.5%; Score 231.5; DB 1; Length 417;
Best Local Similarity 25.3%; Pred. No. 1.8e-09;
Matches 101; Conservative 53; Mismatches 174; Indels 71; Gaps 16;

10 LLLLLLAAALIPFGDGNLFKQVTV-----IGEVATISQV---NKSDDSYQL 58
11 LLLVALVLVSWPPPGTG-----DVVQAPRVGFLGDSVTLPCYQVNMMEVTHVSOL 64
59 L-----NPNRQITPRDFRPLKDRFOLLNFSSELTXTSLTNVS-----ISDEGRYFCQ 167
65 TWAHGESGSMVAHVHQVQPSYSKLEFVAALGAEIRNASIRMGRLAVEBGNVTC- 123
108 LYTDPQDSYTT---ITVLVPPRNIMIDIQKTAVEGESELEV-NCIYMAASKPATIRWEK 163
124 LFTVFPQGRSRVDIWLRLAKPQN-TAEVQR-VQLTGEFVPMARCVSTGCRPPAQITWHS 181
164 GNMKLKGSVEEEM-SDMYTTSQIMLKNHKEDEVAVICQVEHPATGMLQGRYIEVQ 222
182 DLGGPNTSQVPGSLSGVTVTSLMILPSSQVNDGKAVTCVNEHSEKQLLITNLITVY 241
223 YKPOVHQMTPVLOGLTREGDAFELTCEALGKPPVWVWTVYVDDEMPQHAVALSGPVLFT 282

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DB 242 YPPEVSIS-GYDNNRYLQONEA-TLTCDAKSNPEPTGYNNSTMGPLPPRAVAGAOQLI 299
OY 283 NMLNKTDNGYRCASNVIGKASHDYMLYVDPPTTIPPTTTTTTTTTTTTTTTTT 342
DB 300 RVPDPIVITTLICVNTNLGARGAQLFVQVKE-----GPFSEHS----- 338
OY 343 SRAGEGTIGAVDHAIVGVAVVVFAMLCILLIGSYF 381
DB 339 -----GSRNALITVLGILVF--LTLGIGIYF 365

RESULT 10
NTRI_RAT
ID NTRI_RAT STANDARD; PRT; 344 AA.
AC Q62716;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neurotrophin precursor (GP65).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A., AND SEQUENCE OF 217-229.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=95198094; PubMed=7891157;
RA Stryer A.F., Canoll P.D., Wolfgang M.J., Rosen C.L., D'Eustachio P.,
RA Salzer J.L.;
RT "Cloning of neurotrophin defines a new subfamily of differentially
RT expressed neural cell adhesion molecules.";
RL J. Neurosci. 15:2141-2156(1995).
CC -1- FUNCTION: Neural cell adhesion molecule.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -1- TISSUE SPECIFICITY: Central nervous system.
CC -1- DEVELOPMENTAL STAGE: Expressed at high levels in several
CC developing projection systems: in neurons of the thalamus,
CC subplate, and lower cortical laminae in the forebrain and in the
CC pontine nucleus, cerebellar granule cells, and Purkinje cells in
CC the hindbrain.
CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily. IgLON
CC family.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC
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CC
DR EMBL; U16845; AAA67445.1; -.
DR PIR; I56551; I56551.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_C2.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG_Like; 3.
KW Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
KW Repeat; Signal; Lipoprotein.
FT SIGNAL 1 31
FT CHAIN 32 321
FT PROPEP 322 344
FT DOMAIN 39 126
FT DOMAIN 136 218
FT DOMAIN 222 309
FT DISULFID 57 115
FT DISULFID 157 201
FT CARBOHYD 243 295
FT CARBOHYD 44 44
FT CARBOHYD 70 70
FT CARBOHYD 152 152

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FT CARBOHYD 216 216 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 284 284 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 282 282 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 305 305 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 321 321 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT LIPID 321 321 GPI-anchor amidated asparagine (Potential).

SEQUENCE 344 AA; 37998 MW; CBB39BE53B224 CRC64;
 Query Match 10.5%; Score 231; DB 1; Length 344;
 Best Local Similarity 26.2%; Pred. No. 1.5e-09;
 Matches 85; Conservative 56; Mismatches 134; Indels 50; Gaps 15;

QY LLLLLLSAALIPGTG---DQGNLFTK---DVTVEGEVATISCOVNSDSDVLOLNPN 62
 DB LVVVSLRLFLVPTGVPVPSGDAITFPKAMDVTVRQGSATLRCTI---DNRTVRYAMLN 70
 QY 63 RQTI-YRDPFRPLKDSRFQOLNFSSELKVS/LTVNSISDEGRYFCQLYTD-PPQSSYTTI 120
 DB 71 RSTLLVAGNDKWCCLDPRVLLSNQTOYSIEIQNVVDYDEGPYICSVQTDNHPKTSRVHL 130
 QY 121 TVLVPRLMIDIQDITAV-EGEELEVNCTAMASKPATIIRFKNKELKGSVEEMSD 179
 DB 131 IVQVSPK--IVELSSDISNGNNISLTCTIA-TGRPEPTVWRHISPAVGFVSEDEYLE 187
 QY 180 MYTVTSQMLKXVH---KEDGVVPVICOVEHPAVTGNLQTORLEVOYKPOVHIQMTYPLQ 236
 DB 188 ICGITREQSGDEYECASNDVAPVRYVYR-----VTVNPPYIS-----EAK 229
 QY 237 GL-TREGDAFELTCEAIGKPPQVWTVWRVDEMPQ-----HAVLSGPNLFINNLN 286
 DB 230 GTGVVPVGQKGTLOCEASAVPS-AEFQWKDKRLVEGKGVKVENRPLSLTFE--NVS 286
 QY 287 KTDNGTYRCEASNTVGAHSDYMLY 311
 DB 287 EHDYGNVTCVANSNKLGHNTNASIMLF 311

RESULT 11

NTRI HUMAN STANDARD; PRT; 344 AA.
 AC 09P121;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Neurotrophin precursor (hnt).
 GN NT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCB1_Taxid=9606;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Li G., Jin J., Tan X., Yuan J., Qiang B.;
 RT "Cloning and identification of human neurotrophin full length cDNA.";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Neural cell adhesion molecule.
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily. Ig10N family.
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.

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DR EMBL; AF126426; AAF37591.1; -
 DR MIM; 607938; -
 DR GO; GO:0008038; P:neural cell recognition; TAS.

DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_c2.
 DR Pfam; PF00047; Ig_3.
 DR SMART; SM00408; IgC2_2.
 DR PROSITE; PSS0835; IG_Like; 3.
 KW Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
 KW Repeat; Signal; Lipoprotein.

FT SIGNAL 1 31
 FT CHAIN 32 321
 FT PROPEP 322 344
 FT DOMAIN 39 126
 FT DOMAIN 136 218
 FT DOMAIN 222 309
 FT DISULFID 57 115
 FT DISULFID 157 201
 FT DISULFID 243 295
 FT CARBOHYD 44 44
 FT CARBOHYD 70 70
 FT CARBOHYD 152 152
 FT CARBOHYD 284 284
 FT CARBOHYD 292 292
 FT CARBOHYD 305 305
 FT CARBOHYD 321 321
 FT LIPID 321 321
 FT
 SEQUENCE 344 AA; 37971 MW; DA4D12C295ABBE3A CRC64;
 Query Match 10.4%; Score 229; DB 1; Length 344;
 Best Local Similarity 26.3%; Pred. No. 2.1e-09;
 Matches 85; Conservative 57; Mismatches 135; Indels 46; Gaps 15;

QY LLLLLLSAALIPGTG---DQGNLFTK---DVTVEGEVATISCOVNSDSDVLOLNPN 62
 DB LVVVSLRLFLVPTGVPVPSGDAITFPKAMDVTVRQGSATLRCTI---DNRTVRYAMLN 70
 QY 63 RQTI-YRDPFRPLKDSRFQOLNFSSELKVS/LTVNSISDEGRYFCQLYTD-PPQSSYTTI 120
 DB 71 RSTLLVAGNDKWCCLDPRVLLSNQTOYSIEIQNVVDYDEGPYICSVQTDNHPKTSRVHL 130
 QY 121 TVLVPRLMIDIQDITAV-EGEELEVNCTAMASKPATIIRFKNKELKGSVEEMSD 179
 DB 131 IVQVSPK--IVELSSDISNGNNISLTCTIA-TGRPEPTVWRHISPAVGFVSEDEYLE 187
 QY 180 MYTVTSQMLKXVH---KEDGVVPVICOVEHPAVTGNLQTORLEVOYKPOVHIQMTYPLQ 236
 DB 188 ICGITREQSGDEYECASNDVAPVRYVYR-----VTVNPPYIS-----EAK 229
 QY 237 GL-TREGDAFELTCEAIGKPPQVWTVWRVDEMPQ-----HAVLSGPNLFINNLNKT 288
 DB 230 GTGVVPVGQKGTLOCEASAVPS-AEFQWKDKRLVEGKGVKVENRPLSLTFE--NVS 288
 QY 289 DNGTYRCEASNTVGAHSDYMLY 311
 DB 289 DYGNTVTCVANSNKLGHNTNASIMLF 311

RESULT 12

NCM2 MOUSE STANDARD; PRT; 837 AA.
 AC 035136; O35962;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Neural cell adhesion molecule 2 precursor (N-CAM 2) (RB-8 neural cell
 DE adhesion molecule) (R4B12).
 GN NCM2 OR CCAM OR RNCAM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCB1_Taxid=10090;

RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
 RP STRAIN=BALB/c; TISSUE=Olfactory neuroepithelium;
 RC


```

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed most strongly in adult and fetal
CC brain.
CC -1- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC -----
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U75330; AAB80803.1; -.
CC Genbank: H657; NCAM2.
CC MIM: 602040.
CC GO: GO:0016021; C: integral to membrane, TAS.
CC GO: GO:0005886; C: plasma membrane, TAS.
CC GO: GO:0007158; P: neuronal cell adhesion, TAS.
CC InterPro: IPR008957; FN_III-like.
CC InterPro: IPR003961; FN_III.
CC InterPro: IPR007110; IG-like.
CC InterPro: IPR003589; IG_c2.
CC Pfam: PF00041; fn3; 2.
CC SMART: SM00047; IG; 5.
CC SMART: SM00060; FN3; 2.
CC PROSITE: PS50835; IG_LIKE; 5.
CC Cell adhesion; Transmembrane; Glycoprotein; Repeat;
KW Immunoglobulin domain; Signal.
FT SIGNAL 1 19
FT CHAIN 20 837
FT DOMAIN 20 697 NEURAL CELL ADHESION MOLECULE 2.
FT TRANSMEM 698 718 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 719 837 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 837 837
FT DOMAIN 113 108 IG-LIKE C2-TYPE 1.
FT DOMAIN 113 202 IG-LIKE C2-TYPE 2.
FT DOMAIN 208 297 IG-LIKE C2-TYPE 3.
FT DOMAIN 302 396 IG-LIKE C2-TYPE 4.
FT DOMAIN 401 491 IG-LIKE C2-TYPE 5.
FT DOMAIN 482 581 FIBRONECTIN TYPE-III 1.
FT DOMAIN 594 678 FIBRONECTIN TYPE-III 2.
FT DISULFID 42 93 PROBABLE.
FT DISULFID 136 186 PROBABLE.
FT DISULFID 232 281 PROBABLE.
FT DISULFID 322 380 PROBABLE.
FT DISULFID 422 475 PROBABLE.
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 219 219 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 309 309 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 419 419 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 474 474 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 562 562 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 837 AA; 92932 MW; CSD034106C5741C1 CRC64;
Query Match 10.1%; Score 222, DB 1; Length 837;
Best Local Similarity 23.3%; Pred. No. 2,le-08;
Matches 115; Conservative 67; Mismatches 180; Indels 132; Gaps 24;

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QY 184 -TSQMLKXHKEDDGVPIQVEHNAVGNLTQSYLEQYKPKQYHICQTYELOGLTREG 242
DB 262 SNTLETVRNRIINSDGSPYCRATNKA--GEDKQAFLOVFQPHI-IQLK--NETTEN 315
QY 243 DAFELTCENAIKPKQPMVTVVR--VD-----DEMP-----OHAVSGENLFINTIN 286
DB 316 GQTVUCABEGEIP-EITWKAVDGFTPEBCKSPDGRIVEYQGH--GSSSLHIXDKV 371
QY 287 KIDNGTYRCE-ASNYGKASDMLYVY-----DEPTT 318
DB 372 LSGSGRYDEAASRIQGHQKSWYLDIEVAPKEISQTYYSWEGNPINISCDVKANFPAS 431
QY 319 I-----PPPTTTTTTTTTTTTTTTTTTTTTTTTTSRAGEGTICAVDAVIGVAVVFA 369
DB 432 IHWRRKVLPAKNTNLTSTGRKMILEPTSDNDGRYNCATNHTIGRFOEYILA 491
QY 370 MCL-----LIIGRYFAR-----HKGYTFTEAKGADDAADTAIINAEGQ 413
DB 492 LADVPSPYGVXIIIEQTTAKVSEFKPSHGVPDIHHYQVDKVASIWKIVRSHGVO 551
QY 414 -----NNSEKKEY 422
DB 552 TWVYNNLEPNNTTY 565

RESULT 14
NCAL_XENLA STANDARD; PRT; 1092 AA.
ID NCAL_XENLA
AC P36335;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Neural cell adhesion molecule 2, 180 kDa isoform precursor (N-CAM
DE 180).
GN NCAM2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93273239; PubMed=7684721;
RA Tonissen K.F., Kriegl P.A.;
RT "Two neural-cell adhesion molecule (NCAM)-encoding genes in Xenopus
RT laevis are expressed during development and in adult tissues.";
RL Gene 127:243-247(1993).
CC -1- FUNCTION: This protein is a cell adhesion molecule involved in
CC neuron-neuron adhesion, neurite fasciculation, outgrowth of
CC neurites, etc.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=1;
CC Comment=A number of isoforms are produced;
CC Name=1;
CC IsoId=P36335-1; Sequence=Displayed;
CC -1- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M76710; AAA49910.1; -.
CC PIR: JN0635.
CC DR HSSP: P56276; 1TIX.
CC DR InterPro: IPR008957; FN_III-like.
CC DR InterPro: IPR003961; FN_III.

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DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003598; IC2.
DR Pfam: PF0041; fn3, 2.
DR Pfam: PF0047; Ig, 5.
DR SMART: SM0040; FN3, 2.
DR SMART: SM00408; IGC2, 4.
DR PROSITE: PS50835; IG LIKE, 5.
DR Cell adhesion: Glycoprotein; Transmembrane; Repeat;
KW Immunoglobulin domain; Alternative splicing; Signal.
FT SIGNAL 1 19
FT CHAIN 20 1092
FT
FT DOWAIN 20 705
FT TRANSMEM 706 723
FT DOWAIN 724 1092
FT DOWAIN 113 202
FT DOWAIN 208 295
FT DOWAIN 303 397
FT DOWAIN 400 489
FT DOWAIN 512 589
FT DOWAIN 618 686
FT DOWAIN 149 153
FT DOWAIN 158 162
FT DISULFID 41 93
FT DISULFID 136 186
FT DISULFID 232 282
FT DISULFID 323 379
FT DISULFID 420 473
FT CARBOHYD 82 82
FT CARBOHYD 219 219
FT CARBOHYD 310 310
FT CARBOHYD 341 341
FT CARBOHYD 417 417
FT CARBOHYD 443 443
FT CARBOHYD 472 472
SQ SEQUENCE 1092 AA; 118062 MW; CD236E0E8B7AD1 CAC64;

Query Match 10.1%; Score 222; DB 1; Length 1092;
Best Local Similarity 23.9%; Pred. No. 2.9e-08;
Matches 81; Conservative 66; Mismatches 150; Indels 40; Gaps 15;

Cy 32 KDVIIVGEVATISC---QVTKS---DDSVIQLN---PNRQIYPRDPRLKDSRFL 81
Db 199 KDVIIVNVPPLIQAQRIVNATAMDESIVLSCDADGFPDPRLSMKKEPIEDGB-ER 257
Cy 82 LNFSSSELKVSILNVISISDEGRYFCQLYTDPQESYTTITVLVPPNLMIDIQDTAVSG 141
Db 258 ISFNEKSEMTIYVEKEDEDAEYSC-IANNQAGEAIVLKYAKPKMTYVENKTTVEH 316
Cy 142 EEIVNCTAMSKATITRMFKNGKELKGSEVEEMSDMTVT-----SQLMKVHKED 195
Db 317 DEITLTCEA-SGDIPISITWTRAKNI---SSEKTLIDGHIVVKDHIMSALTIKOIQT 372
Cy 196 DGEVVICQVEHPAVTGNLQOTRYLEVOYKPOVHIQMTYPLQGLTREGDAEELTCEAIKGR 255
Db 373 DAGEYFVCAVNP-IGVDMQAM-YFEVQYAPKIR---GPVVVYTWESNPVNICDVIAHF 426
Cy 256 QPVAVTVKRVDDENPQH-----AVLSGP---NLFINLAKTIDNGTGRCEASNVGCAHSD 307
Db 427 S-AAVSWFRDQQLPSSNFSNINIKYNPTSSLEVNDSSNDGNCVNSIGHSSE 485
Cy 308 YMLVYDPEPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 346
Db 486 FILVQADLPSS---PAIRKVEPYSYTWIVFDESDAIGG 521

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DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Nephrit precursor (Renal glomerulus-specific cell adhesion receptor).
GN NPHS1 OR NPHN
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. AND SUBCELLULAR LOCATION.
RX MEDLINE=99436145; PubMed=10504499;
RA Holman L.B., St John P.L., Kovari I.A., Verma R., Holtsoefer H.,
RA Abrahamson D.R.;
RT "Nephrit localizes to the slit pore of the glomerular epithelial
RT cell."
RT Kidney Int. 56:1481-1491(1999).
RN [2]
RP INTERACTION WITH CD2AP.
RX MEDLINE=21590051; PubMed=11733379;
RA Shih N.-Y., Li J., Cotran R., Mundel P., Miner J.H., Shaw A.S.;
RT "CD2AP localizes to the slit diaphragm and binds to nephrit via a
RT novel C-terminal domain."
RT Am. J. Pathol. 159:2303-2308(2001).
RN [3]
RP INTERACTION WITH CD2AP AND NPHS2.
RX MEDLINE=21590460; PubMed=11733557;
RA Schwarz K., Simons W., Reiser U., Saleem M.A., Paul C., Kriz W.,
RA Shaw A.S., Holzman L.B., Mundel P.;
RT "Podocin, a raft-associated component of the glomerular slit
RT diaphragm, interacts with CD2AP and nephrit."
RT J. Clin. Invest. 108:1621-1629(2001).
RN [4]
RP FUNCTION: Seems to play a role in the development or function of
RP the kidney glomerular filtration barrier. May anchor the podocyte
RP slit diaphragm to the actin cytoskeleton.
RP - SUBUNIT: Interacts with podocin/NPHS2 and with CD2AP C-terminal
RP domain.
RP - SUBCELLULAR LOCATION: Type I membrane protein (Potential). Located
RP at podocyte slit diaphragm between podocyte foot processes.
RP - TISSUE SPECIFICITY: Expressed in kidney glomeruli.
RP - PTM: Phosphorylated on tyrosine residues (by similarity).
RP - SIMILARITY: Belongs to the immunoglobulin superfamily.
RP - SIMILARITY: Contains 8 immunoglobulin-like domains.
RP - SIMILARITY: Contains 1 fibronectin type III domain.
RP -----
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RP or send an email to license@isb-sib.ch).
RP -----
CC EMBL: AF168466; AAF03368.1;
CC GDB: MGI:1859637; Nphs1.
CC GO: GO:0005515; F:protein binding; IPI.
CC GO: GO:0007254; P:JNK cascade; IDA.
CC GO: GO:0000165; P:MAPKK cascade; IDA.
CC InterPro: IPR008957; FN III-like.
CC InterPro: IPR003961; FN III.
CC InterPro: IPR007110; IG-like.
CC InterPro: IPR003598; IC2.
CC Pfam: PF0041; fn3, 1.
CC Pfam: PF0047; Ig, 8.
CC SMART: SM0040; FN3, 1.
CC SMART: SM00408; IGC2, 1.
CC PROSITE: PS50835; IG LIKE; 8.
KW Cell adhesion; Transmembrane; Signal; Glycoprotein;
KW Immunoglobulin domain; Repeat; Phosphorylation.
FT SIGNAL 1 22
FT CHAIN 23 1242
FT DOWAIN 23 1064
FT TRANSMEM 1065 1086
FT DOWAIN 1087 1242
FT DOWAIN 125 130

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FT DOMAIN 135 233 IG-LIKE C2-TYPE 2.
FT DOMAIN 242 333 IG-LIKE C2-TYPE 3.
FT DOMAIN 340 434 IG-LIKE C2-TYPE 4.
FT DOMAIN 440 540 IG-LIKE C2-TYPE 5.
FT DOMAIN 544 635 IG-LIKE C2-TYPE 6.
FT DOMAIN 740 832 IG-LIKE C2-TYPE 7.
FT DOMAIN 838 939 IG-LIKE C2-TYPE 8.
FT DOMAIN 941 1025 FIBROECTIN TYPE-III.
FT DISULFID 53 111 POTENTIAL.
FT DISULFID 160 217 POTENTIAL.
FT DISULFID 265 317 POTENTIAL.
FT DISULFID 361 417 POTENTIAL.
FT DISULFID 465 528 POTENTIAL.
FT DISULFID 567 623 POTENTIAL.
FT DISULFID 761 816 POTENTIAL.
FT DISULFID 863 920 POTENTIAL.
FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 547 547 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 553 553 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 564 564 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 577 577 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 680 680 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 708 708 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 908 908 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1242 AA; 134890 MW; 02D82180BF145092 CRC64;
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Query Match 10.1%; Score 221; DB 1; Length 1242;

Best Local Similarity 22.7%; Pred. No. 4e-08; Matches 86; Conservative 75; Mismatches 164; Indels 54; Gaps 16;

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QY 5 GLRLRLLLLSAALIPTEGDN-----LFTKDVYIEGEVATISCCQNKSD 53
Db 4 GTTLRASILL--AGMLTGTGAQSPVPSADRGFWALSENLTVEGSTIKLMGCV-RAPG 59
QY 54 SVIQ-----LLNPNRQTIYFRDRPLKDSRFQULNFSSSEKLKSLTNVSIIDGRYFCQ 107
Db 60 SVVQWAKDGLLLGNPKIPGFPRYSLEGDS-----AKGEFHLLIEACDLSDAEYECQ 112
QY 108 LYTP--PQ--ESYTTITVLPNNLMIDIOKD--TAVEGEIEVNCIAMSAPATTIR 160
Db 113 VGRSEIGSELYSPRVILSVLPKVLQUTPEAGSTVTVWAGERYVTCSGAKAPDII 172
QY 161 WFKGNKEIKG-KSEVEKSD--MYTVSQMLKVKHEDDGVPIQVEHPAVTGNLQTOR 217
Db 173 FIQGRIVEDVSSSVNEGSEKELFTEFAEAVTPQSSDNGQLVCEGSPALATPIKASF 232
QY 218 YLEVOYKQVHIOMTYP--LQGLTREGAPFLTCEAIGKPPVAVTVVRVDDEM-----P 270
Db 233 TMAILFPFGPPV-IDWPGINAGHVRAGENLELPCTIARGNPPATLQWLKNGKPYSIAMGT 291
QY 271 QHAAVLSGNLFINNLNKTNDGT-YRCEASNIIVGKAHSDMYLYYDPPPTIIPPTT----- 325
Db 292 EHAQAVASHVLYMTVRPEDHGARLSCQSYNSVSAETQERSITL---QVTFPPSAVTIIGS 348
QY 326 TTTTITTTTITLITITDSR 344
Db 349 TSGSEKNKVTLLCCLTKSR 367
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Search completed: July 7, 2004, 06:03:55
Job time : 29.874 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 7, 2004, 05:56:13 ; Search time 59.1711 Seconds

(without alignments)
2255.564 Million cell updates/sec

Title: US-10-622-237-4

Perfect score: 2197

Sequence: 1 AAPPGRLRLRLLLLSAAL.....TAIINAGGQNNSEKXEYF 423

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries
SPTREMBL.25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2197	100.0	445	11	Q8R4L1 mus musculus
2	2193	99.8	445	11	Q8R3T6 mus musculus
3	2176.5	99.1	445	11	Q8R3M8 mus musculus
4	2166	98.6	442	4	Q9BY67 mus sapien
5	2027	92.3	417	11	Q7TMD1 mus musculus
6	2020.5	92.0	443	4	Q8N2P4 mus sapien
7	1631	74.2	336	11	Q9DCE7 mus musculus
8	1631	74.2	336	11	Q80V44 mus musculus
9	1615	73.5	333	4	Q86WR8 mus sapien
10	1546	70.4	295	11	Q9Z2H8 mus musculus
11	1513.5	68.9	306	11	Q9QYL4 mus musculus
12	1493	68.0	295	11	Q9QYL6 mus musculus
13	1404	63.9	289	11	Q9QYL6 mus musculus
14	1380.5	62.8	278	11	Q9QYL3 mus musculus
15	897	40.8	435	4	Q8N3J6 mus sapien
16	895	40.7	437	4	Q8I2P8 mus sapien

17	864	39.3	404	11	Q8BLQ9 mus musculus
18	860	39.1	404	11	Q8BYL1 mus musculus
19	857	39.0	395	11	Q8BXJ7 mus musculus
20	854	38.9	395	11	Q8BZP4 mus musculus
21	800	36.4	394	13	Q7ZXX1 xenopus lae
22	766.5	34.5	388	4	Q8NFZ8 mus sapien
23	757.5	34.5	388	11	Q8R4E4 mus musculus
24	739.5	33.7	396	11	Q9N2M8 mus musculus
25	732.5	33.3	398	4	Q8N1Z6 mus sapien
26	730.5	33.2	381	4	Q9Y4A4 mus sapien
27	715.5	32.6	432	4	Q9UPL1 mus sapien
28	371.5	16.9	163	11	Q8L1H8 mus musculus
29	362.5	16.5	163	4	Q9NVJ5 mus sapien
30	360.5	16.4	152	11	Q8BSQ8 mus musculus
31	337.5	15.4	549	11	Q9D006 mus musculus
32	334.5	15.2	549	11	Q9JL39 mus musculus
33	325.5	14.8	549	4	Q9N0S3 mus sapien
34	323.2	14.7	234	4	Q8I2Q9 mus sapien
35	303.5	13.8	438	11	Q9JLB7 mus musculus
36	303.5	13.8	510	11	Q9JLB8 mus musculus
37	283	12.9	439	13	Q57349 gallus gall
38	270	12.3	407	4	Q9Y4I2 mus sapien
39	263	12.0	1482	5	Q9Y4Y0 drosophila
40	261.5	11.9	5175	5	Q8I0I3 caenorhabd
41	261.5	11.9	5198	5	Q76S18 mus sapien
42	248.5	11.3	624	11	Q8C1J4 mus musculus
43	248.5	11.3	789	11	Q80W68 mus musculus
44	247.5	11.3	467	11	Q91VT9 mus musculus
45	247.5	11.3	510	4	Q96NYS mus sapien

ALIGNMENTS

RESULT 1
Q8R4L1 PRELIMINARY; PRT; 445 AA.
AC Q8R4L1;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Tumor suppressor in lung cancer 1.
GN IGSP4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Svj.
RA Fukami T., Maruyama T., Murakami Y.,
RT "Identification of murine orthologue of the TSUC1 gene."
RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF434663; AL86736.1; -
DR MGD; MGI:1889272; IGsf4.
DR GO; GO:0045202; C:synaptic junction; IDA.
DR GO; GO:008021; C:synaptic vesicle; IDA.
DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . . ; IDA.
DR GO; GO:000515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR GO; GO:0007416; P:synaptogenesis; IDA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG-C2.
DR InterPro; IPR003585; Neurexin-like.
DR Pfam; PR00047; ig_3.
DR SMART; SM00294; 4.1m; 1.
DR SMART; SM00408; IgC2; 1.
DR PROSITE; PS00835; IG-LIKE; 3.
KW Immunoglobulin domain.
SQ
SEQUENCE 445 AA; 48664 MW; CSD5A070DAF70E55 CRC64;
Query Match 100.0%; Score 2197; DB 11; Length 445;
Best Local Similarity 100.0%; Pred. No. 7.3e-178;

Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 AAPPGLRLRLLLLSAAALIPFGDGNLFTKDVTVIEGVATISCCVNSKSDSVIQLLN 60
D 22 AAPPGLRLRLLLLSAAALIPFGDGNLFTKDVTVIEGVATISCCVNSKSDSVIQLLN 81
QY 61 PNRCTIYFRDPRPKDSRFQQLNFSSELKVSILTVNISDEGRYFCQLYTDPPQESYTTI 120
D 82 PNRCTIYFRDPRPKDSRFQQLNFSSELKVSILTVNISDEGRYFCQLYTDPPQESYTTI 141
QY 121 TVLPPRLMLIDIKOTAVEGEIEVNCSTAMASKPATIIRPFKNKELKXKSEVEWSDM 180
D 142 TVLPPRLMLIDIKOTAVEGEIEVNCSTAMASKPATIIRPFKNKELKXKSEVEWSDM 201
QY 181 YTTVSQLMLKXHKEDDGPVTCQVEHPAVTGNLQTORYLEVQYKPOVHIQMTYPLQGLTR 240
D 202 YTTVSQLMLKXHKEDDGPVTCQVEHPAVTGNLQTORYLEVQYKPOVHIQMTYPLQGLTR 261
QY 241 EGDAPFELTCEAIGKPOVMTWVAVDEMPQHAVLGSPNLFINNLTNGTYRCEASNI 300
D 262 EGDAPFELTCEAIGKPOVMTWVAVDEMPQHAVLGSPNLFINNLTNGTYRCEASNI 321
QY 301 VGKASDYMALVYDPTTIPPTTTTTTTTTTTTTTTTTTTTTTDSRAGEEGTIGAVDHAIVG 360
D 322 VGKASDYMALVYDPTTIPPTTTTTTTTTTTTTTTTTTTTTTDSRAGEEGTIGAVDHAIVG 381
QY 361 GVAVVVFAMLCILIIIGRYFARHKGTYFTHAKGADADADADATAIINAGGONNSEKK 420
D 382 GVAVVVFAMLCILIIIGRYFARHKGTYFTHAKGADADADADATAIINAGGONNSEKK 441
QY 421 EYF 423
D 442 EYF 444

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RESULT 2

```

Q8K3T6 PRELIMINARY; PRT; 445 AA.
ID Q8K3T6
AC Q8K3T6;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE SynCAM, a synaptic adhesion molecule that drives synapse assembly."
GN IGSF4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/
RA Biederer T., Sara Y., Mozhayeva M., Atasoy D., Liu X., Kavalali E.T.,
RA Sudhof T.C.;
RT "SynCAM, a synaptic adhesion molecule that drives synapse assembly."
RT Science 0:0-0(2002).
RL EMBL; AF539424; L4N01614.1; -.
DR MGD; MGI:1889272; Igsf4.
DR GO; GO:0045202; C:synaptic junction; IDA.
DR GO; GO:0008021; C:synaptic vesicle; IDA.
DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . ; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR GO; GO:0007416; P:synaptogenesis; IDA.
DR InterPro; IPR003599; I9.
DR InterPro; IPR007110; I9-like.
DR InterPro; IPR003598; I9_c2.
DR Pfam; PF00047; I9; 3.
DR SMART; SM00409; IGC2; 3.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS50835; I9-LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 445 AA; 4866 MW; 5B36F23F1877497 CRC64;

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Query Match 99.8%; Score 2193; DB 11; Length 445;
 Best Local Similarity 99.8%; Pred. No. 1.6e-177;
 Matches 423; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AAPPGLRLRLLLLSAAALIPFGDGNLFTKDVTVIEGVATISCCVNSKSDSVIQLLN 60
D 22 AAPPGLRLRLLLLSAAALIPFGDGNLFTKDVTVIEGVATISCCVNSKSDSVIQLLN 81
QY 61 PNRCTIYFRDPRPKDSRFQQLNFSSELKVSILTVNISDEGRYFCQLYTDPPQESYTTI 120
D 82 PNRCTIYFRDPRPKDSRFQQLNFSSELKVSILTVNISDEGRYFCQLYTDPPQESYTTI 141
QY 121 TVLPPRLMLIDIKOTAVEGEIEVNCSTAMASKPATIIRPFKNKELKXKSEVEWSDM 180
D 142 TVLPPRLMLIDIKOTAVEGEIEVNCSTAMASKPATIIRPFKNKELKXKSEVEWSDM 201
QY 181 YTTVSQLMLKXHKEDDGPVTCQVEHPAVTGNLQTORYLEVQYKPOVHIQMTYPLQGLTR 240
D 202 YTTVSQLMLKXHKEDDGPVTCQVEHPAVTGNLQTORYLEVQYKPOVHIQMTYPLQGLTR 261
QY 241 EGDAPFELTCEAIGKPOVMTWVAVDEMPQHAVLGSPNLFINNLTNGTYRCEASNI 300
D 262 EGDAPFELTCEAIGKPOVMTWVAVDEMPQHAVLGSPNLFINNLTNGTYRCEASNI 321
QY 301 VGKASDYMALVYDPTTIPPTTTTTTTTTTTTTTTTTTTTTTDSRAGEEGTIGAVDHAIVG 360
D 322 VGKASDYMALVYDPTTIPPTTTTTTTTTTTTTTTTTTTTTTDSRAGEEGTIGAVDHAIVG 381
QY 361 GVAVVVFAMLCILIIIGRYFARHKGTYFTHAKGADADADADATAIINAGGONNSEKK 420
D 382 GVAVVVFAMLCILIIIGRYFARHKGTYFTHAKGADADADADATAIINAGGONNSEKK 441
QY 421 EYF 423
D 442 EYF 444

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RESULT 3

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Q8R5M8 PRELIMINARY; PRT; 456 AA.
ID Q8R5M8
AC Q8R5M8;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE RAI175.
GN IGSF4 OR RAI175.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_Taxid=10090;
RX [1]
RN SEQUENCE FROM N.A.
RP Monoclonal T.
RA "Biological function of RAI175, a new member of immunoglobulin super
RA family."
RT Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
RL EMBL; AB064265; BAB83501.2; -.
DR MGD; MGI:1889272; Igsf4.
DR GO; GO:0045202; C:synaptic junction; IDA.
DR GO; GO:0008021; C:synaptic vesicle; IDA.
DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . ; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR GO; GO:0007416; P:synaptogenesis; IDA.
DR InterPro; IPR007110; I9-like.
DR InterPro; IPR003598; I9_c2.
DR InterPro; IPR003585; Neurexin-like.
DR Pfam; PF00047; I9; 3.
DR SMART; SM00294; 4.1m; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; I9-LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 456 AA; 49787 MW; 322E866A4BC1C7F CRC64;

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RESULT 4			
ID	Q9BY67	PRELIMINARY;	PRT; 442 AA.
AC	Q9BY67;		
DT	01-JUN-2001 (T-EMBLrel. 17, Created)		
DT	01-JUN-2001 (T-EMBLrel. 17, Last sequence update)		
DT	01-OCT-2003 (T-EMBLrel. 25, Last annotation update)		
DE	Nectin-like protein 2.		
GN	NECL2.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Zhou Y., Du G., Chen J., Yuan J., Qiang B.;		
RT	"Cloning of a novel human cDNA encoding a member of the immunoglobulin		
RT	superfamily,";		
RL	Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF132811; AAF69029.1; -		
DR	Gene; HGNC:5951; IGSF4.		
DR	InterPro; IPR007110; IG-1-like.		
DR	InterPro; IPR003598; IG_C2.		
DR	InterPro; IPR003585; Neutxin-like.		
DR	Pfam; PF00047; IG_3.		
DR	SMART; SM00294; 4.1m; 1.		
DR	SMART; SM00408; IGC2; 1.		
DR	PROSITE; PS50835; IG_LIKE; 3.		
KM	Immunoglobulin domain.		
SC	SEQUENCE 442 AA; 48537 MW; 68183E323875062 CRC64;		

Query Match	98.6%;	Score 2166;	DB 4;	Length 442;
Best Local Similarity	98.6%;	Pred. No. 3.1e-175;		
Matches 417;	Conservative	2;	Mismatches 4;	Indels 0;
			Gaps	0

RESULT	5
027NLT1	
ID	027NLT1
AC	PRELIMINARY;
PRT	417 AA.
DT	01-OCT-2003 (TREMBlrel. 25, Created)
DT	01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT	01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE	Nectin-like molecule 2.
OS	Mus musculus (Mouse).
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxId=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6; TISSUE=Brain;
RA	Shingai T., Ikeda T., Kakunaga S., Morimoto K., Takekuni K., Itoh S.,
RA	Sato K., Takeuchi M., Imai T., Monden M., Takai Y.;
RT	"Implications of nectin-like molecule
RT	2/IGSF4/RA175/StrGSP/msc1/SyngCm1 in cell-cell adhesion and
RT	transmembrane protein localization in epithelial cells.",
RL	J Biol Chem 270:0-0(2003).
EQ	EXBL: A135136; AA02381.
Q	SEQUENCE 417 AA; 45779 MW; 98500160D37845C2 CRC64;

Query Match	92.3%;	Score 2027;	DB 11;	Length 417;
Best Local Similarity	93.4%;	Pred. No. 1.8e-163;		
Matches 395;	Conservative 0;	Mismatches 0;	Indels 28;	Gaps 1

QY	1AAPPGGIRRLILLILISAALILPTGDGQNLFKDVTVEGSAATISCVNKSDDSVIQLLN	60
Db	22AAPGGIRRLILLILISAALILPTGDGQNLFKDVTVEGSAATISCVNKSDDSVIQLLN	81
QY	61PKRQITVEADRRPLKDSFQOLLNFSSESEKXSLTNVISISEGGYFCOLYTPDPQESYTI	120
Db	82PKRQITVEADRRPLKDSFQOLLNFSSESEKXSLTNVISISEGGYFCOLYTPDPQESYTI	141
QY	121TVLVPRRLMLMDIQKTAIVSGEELVONCTAMASKPATITWFKGNELKSGKSEVESMD	180
Db	142TVLVPRRLMLMDIQKTAIVSGEELVONCTAMASKPATITWFKGNELKSGKSEVESMD	201

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QY 181 YVTSQMLTKVHKEDDGVPIQVEHPAVTGNLQOTRYLEVQYKQVHIQMTYPLQGLTR 240
DB 202 YVTSQMLTKVHKEDDGVPIQVEHPAVTGNLQOTRYLEVQYKQVHIQMTYPLQGLTR 261
QY 241 EGSAPFELTCAIGKPPQVMTWVRVDEMPQHAVLSGPNLFNNKNTKNDNGYRCEASNI 300
DB 262 EGSAPFELTCAIGKPPQVMTWVRVDEMPQHAVLSGPNLFNNKNTKNDNGYRCEASNI 321
QY 301 VGKASDYMMLVYDPTTTPPTTTTTTTTTTTTTTTTTTTTTTSRAGEECTIGAVDHAIVG 360
DB 322 VGKASDYMMLVYDPTTTPPTTTTTTTTTTTTTTTTTTTTTTSRAGEECTIGAVDHAIVG 353
QY 361 GVAVAVVFMMLCLLIIIGRYFARHKGTFTHEAKGADDAADDTAIINAGGONNSEEK 420
DB 354 GVAVAVVFMMLCLLIIIGRYFARHKGTFTHEAKGADDAADDTAIINAGGONNSEEK 413
QY 421 EYF 423
DB 414 EYF 416

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RESULT 6

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Q8N2F4 PRELIMINARY; PRT; 443 AA.
AC O8N2F4;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Hypothetical protein HEMBA1001879.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayaishi K., Ishii S.,
RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
RA Nagahari K., Sugano S., Isogai T.;
RT "HRI human cDNA sequencing project.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK075502; BAC11657.1; -
DR InterPro; IPR003599; Ig_
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00409; Ig_3.
DR SMART; SM00408; IgC2; 3.
DR PROSITE; PS50835; Ig_LIKE; 3.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 443 AA; 48648 MW; 046B43AA156F6F64 CRC64;

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Query Match 92.0%; Score 2020.5; DB 4; Length 443;
Best Local Similarity 92.9%; Pred. No. 6; 9e-163;
Matches 394; Conservative 5; Mismatches 24; Indels 1; Gaps 1;
QY 1 AAPPGLRLRLLLLSAALIPITGQGNLFPTKVTYIEGVAITSCVKNKSDSVYQLLN 60
DB 19 AAPPGLRLRLLLLSAALIPITGQGNLFPTKVTYIEGVAITSCVKNKSDSVYQLLN 78
QY 61 PNRQTIYFRDPRPKDSRFQNLNFSSELKVLNVSISDEGRYFQCLYDPPQESYTTI 120
DB 79 PNRQTIYFRDPRPKDSRFQNLNFSSELKVLNVSISDEGRYFQCLYDPPQESYTTI 138
QY 121 TVLVPRNLMIDIOKDTAVEGEIEVACTAMASPKATITWFKGNKELKSKSEVEEWSDM 180
DB 139 TVLVPRNLMIDIOKDTAVEGEIEVACTAMASPKATITWFKGNKELKSKSEVEEWSDM 198
QY 181 YVTSQMLTKVHKEDDGVPIQVEHPAVTGNLQOTRYLEVQYKQVHIQMTYPLQGLTR 240
DB 199 YVTSQMLTKVHKEDDGVPIQVEHPAVTGNLQOTRYLEVQYKQVHIQMTYPLQGLTR 258
QY 241 EGSAPFELTCAIGKPPQVMTWVRVDEMPQHAVLSGPNLFNNKNTKNDNGYRCEASNI 300

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DB 259 EGDALFELTCAIGKPPQVMTWVRVDEMPQHAVLSGPNLFNNKNTKNDNGYRCEASNI 318
QY 301 VGKASDYMMLVYDPTTTPPTTTTTTTTTTTTTTTTTTTTTTSRAGEECTIGAVDHAIVG 359
DB 319 VGKASDYMMLVYDPTTTPPTTTTTTTTTTTTTTTTTTTTTTSRAGEECTIGAVDHAIVG 378
QY 360 GVAVAVVFMMLCLLIIIGRYFARHKGTFTHEAKGADDAADDTAIINAGGONNSEEK 419
DB 379 GVAVAVVFMMLCLLIIIGRYFARHKGTFTHEAKGADDAADDTAIINAGGONNSEEK 438
QY 420 KEYF 423
DB 439 KEYF 442

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RESULT 7

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Q9D6E7 PRELIMINARY; PRT; 336 AA.
AC Q9D6E7;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE 2900073G06R1K protein.
GN IGSP4 OR 2900073G06R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schiml L.M., Stanbii F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baidarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carinci P., de Bonaldo M.F.,
RA Bustinich S., Hill D., Hofmann M., Hune D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima U., Mazzaletti U., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilting L.,
RA Wymshar-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohseki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 403:685-690(2001).
DR EMBL; AK013775; BAB28988.1; -
DR MGD; MGI:1889272; IgSf4.
DR GO; GO:0045202; C:synaptic junction; IDA.
DR GO; GO:0008021; C:synaptic vesicle; IDA.
DR GO; GO:0016347; F:calcium independent cell adhesion molecule . . . ; IDA.
DR GO; GO:0005515; F:protein binding; IPT.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR GO; GO:0007416; P:synaptogenesis; IDA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00408; IgC2; 1.
DR PROSITE; PS50835; Ig_LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 336 AA; 37157 MW; FP887FA4EFDF120 CRC64;

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Query Match 74.2%; Score 1631; DB 11; Length 336;
Best Local Similarity 100.0%; Pred. No. 5; 3e-130;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AAPGLRLRLRLRLRLRLSAALIPITGDSQNLFTKDVTVIEGEVATISCCVNKSDSDSVIQLLN 60
Db 22 AAPGLRLRLRLRLRLRLSAALIPITGDSQNLFTKDVTVIEGEVATISCCVNKSDSDSVIQLLN 81
QY 61 PNRQTIYFRDRPLKDSRFQLLNFSSSELKVSILTNVSIISDEGRYFCQLYTPDPQESYTTI 120
Db 82 PNRQTIYFRDRPLKDSRFQLLNFSSSELKVSILTNVSIISDEGRYFCQLYTPDPQESYTTI 141
QY 121 TVLVPRLMLTIDIQDITAVEGEIEVNCCTAMASKPATITIRFWKGNKELKGSEVEBMSDM 180
Db 142 TVLVPRLMLTIDIQDITAVEGEIEVNCCTAMASKPATITIRFWKGNKELKGSEVEBMSDM 201
QY 181 YTVTSQMLKVKHKEDDGVPICOVEHPAVTGNLTQORYLEVOYKPOVHIQMTYPLQGLTR 240
Db 202 YTVTSQMLKVKHKEDDGVPICOVEHPAVTGNLTQORYLEVOYKPOVHIQMTYPLQGLTR 261
QY 241 EGDAPFELTCEAIGKQPQVMTWVRVDEMPQHAVALSGPNLFINNLKNTDNGTYRCEASNI 300
Db 262 EGDAPFELTCEAIGKQPQVMTWVRVDEMPQHAVALSGPNLFINNLKNTDNGTYRCEASNI 321
QY 301 VGKAHSDYMLYVY 313
Db 322 VGKAHSDYMLYVY 334

RESULT 8
Q80VG4 ID 080VG4 PRELIMINARY; PRT; 336 AA.
AC 080VG4;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE A secretion form of SgISGF/TSIC1.
GN SgISGF/TSIC1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Spleen cell-derived;
RA Ito A., Koma Y., Nagano T.;
RT "A secretion form of SgISGF/TSIC1."
RL Submitted (SMP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB092414; BAC6173.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00409; IgC2; 3.
DR SMART; SM00408; IgC2; 3.
DR PROSITE; PSS0835; IG_LIKE; 3.
SQ SEQUENCE 336 AA; 3715 MW; 9EF3D8B8BE5E8F72 CRC64;

Query Match 74.2%; Score 1631; DB 11; Length 336;
Best Local Similarity 100.0%; Pred. No. 5.3e-130;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 241 EGDAPFELTCEAIGKQPQVMTWVRVDEMPQHAVALSGPNLFINNLKNTDNGTYRCEASNI 300
Db 262 EGDAPFELTCEAIGKQPQVMTWVRVDEMPQHAVALSGPNLFINNLKNTDNGTYRCEASNI 321
QY 301 VGKAHSDYMLYVY 313
Db 322 VGKAHSDYMLYVY 334

RESULT 9
Q86WB8 ID 086WB8 PRELIMINARY; PRT; 333 AA.
AC 086WB8;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Secretory isoform of TSIC-1.
GN TSIC-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Ito A., Koma Y., Nagano T.;
RT "Cloning of a secretory isoform of SgISGF/TSIC-1."
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB094146; BAC6178.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00409; Ig; 3.
DR SMART; SM00408; IgC2; 3.
DR PROSITE; PSS0835; IG_LIKE; 3.
SQ SEQUENCE 333 AA; 36915 MW; D7C1102F46D08492 CRC64;

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Query Match 73.5%; Score 1615; DB 4; Length 333;
Best Local Similarity 99.0%; Pred. No. 1.2e-128;
Matches 310; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAPGLRLRLRLRLRLSAALIPITGDSQNLFTKDVTVIEGEVATISCCVNKSDSDSVIQLLN 60
Db 19 AAPGLRLRLRLRLRLSAALIPITGDSQNLFTKDVTVIEGEVATISCCVNKSDSDSVIQLLN 78
QY 61 PNRQTIYFRDRPLKDSRFQLLNFSSSELKVSILTNVSIISDEGRYFCQLYTPDPQESYTTI 120
Db 79 PNRQTIYFRDRPLKDSRFQLLNFSSSELKVSILTNVSIISDEGRYFCQLYTPDPQESYTTI 138
QY 121 TVLVPRLMLTIDIQDITAVEGEIEVNCCTAMASKPATITIRFWKGNKELKGSEVEBMSDM 180
Db 139 TVLVPRLMLTIDIQDITAVEGEIEVNCCTAMASKPATITIRFWKGNKELKGSEVEBMSDM 198
QY 181 YTVTSQMLKVKHKEDDGVPICOVEHPAVTGNLTQORYLEVOYKPOVHIQMTYPLQGLTR 240
Db 199 YTVTSQMLKVKHKEDDGVPICOVEHPAVTGNLTQORYLEVOYKPOVHIQMTYPLQGLTR 258
QY 241 EGDAPFELTCEAIGKQPQVMTWVRVDEMPQHAVALSGPNLFINNLKNTDNGTYRCEASNI 300
Db 259 EGDAPFELTCEAIGKQPQVMTWVRVDEMPQHAVALSGPNLFINNLKNTDNGTYRCEASNI 318
QY 301 VGKAHSDYMLYVY 313
Db 319 VGKAHSDYMLYVY 331

RESULT 10
Q92ZB8 ID 092ZB8 PRELIMINARY; PRT; 295 AA.
AC 092ZB8;
DT 01-MAY-1999 (TREMBlrel. 10, Created)

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DT 01-MAY-1999 (T-EMBLrel. 10, last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, last annotation update)
 DE Nectin-like protein 2.
 GN IGSF4 OR NECT2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RX [1]
 RN SEQUENCE FROM N.A.
 RA Zhou Y., Du G., Chen J., Yuan J., Qiang B.;
 RT "Cloning of a novel cDNA encoding a member of immunoglobulin family";
 RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF061260; AAC67243.1; -
 DR MGD; MGI:1889272; Igsf4.
 DR GO; GO:0045202; C:synaptic junction; IDA.
 DR GO; GO:0008021; C:synaptic vesicle; IDA.
 DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . .; IDA.
 DR GO; GO:0005515; F:protein binding; IPT.
 DR GO; GO:0007155; P:cell adhesion; IDA.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003598; IG_C2.
 DR InterPro: IPR003585; Neurexin-like.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00294; 4.1m; 1.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 295 AA; 32509 MW; 9DE9D86F6F6F48 CRC64;
 Query Match 70.4%; Score 1546; DB 11; Length 295;
 Best Local Similarity 100.0%; Pred. No. 7.2e-123;
 Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 130 MIDIQKTAVGEIEVNCCTAMASKPATITRMFKNGKELGKSEVEWSDMTVTTSQML 189
 DB 1 MIDIQKTAVGEIEVNCCTAMASKPATITRMFKNGKELGKSEVEWSDMTVTTSQML 60
 QY 190 KVKHEDGVPIQCVHEPAVTGNLQTORYLEVOYKPOVHIQMTYPLQGLTRGDAPFLTC 249
 DB 61 KVKHEDGVPIQCVHEPAVTGNLQTORYLEVOYKPOVHIQMTYPLQGLTRGDAPFLTC 120
 QY 250 EAIKGPQVWVTWVRVDDEMPQHAVALSGPMLFINNKNKTNGTYRCESNIVGKAHSDYM 309
 DB 121 EAIKGPQVWVTWVRVDDEMPQHAVALSGPMLFINNKNKTNGTYRCESNIVGKAHSDYM 180
 QY 310 LYVVDPTTTPPTTTTTTTTTTTTTTTTTTTTTTTTTTDSRAGEEGTIGAVDHAIVGVAVVFA 369
 DB 181 LYVVDPTTTPPTTTTTTTTTTTTTTTTTTTTTTTTTTDSRAGEEGTIGAVDHAIVGVAVVFA 240
 QY 370 MLCILITLGRYFAHKGTYFTHAKGADDAADDTALINAGGONNSEKKYF 423
 DB 241 MLCILITLGRYFAHKGTYFTHAKGADDAADDTALINAGGONNSEKKYF 294
 RESULT 11
 QOXYL4 PRELIMINARY; PRT; 306 AA.
 AC QOXYL4;
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, last annotation update)
 DE Adhesion protein RA175C.
 GN IGSF4 OR RA175C.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RX [1]
 RN SEQUENCE FROM N.A.
 RA Soyama A., Fujita E., Urabe K., Mukasa T., Kourouku Y., Momoi M.,
 Momoi T.;

RT "RA175, a novel neuron specific adhesion protein.",
 RL Submitted (Dec-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB021966; BAA87916.1; -
 DR MGD; MGI:1889272; Igsf4.
 DR GO; GO:0045202; C:synaptic junction; IDA.
 DR GO; GO:0008021; C:synaptic vesicle; IDA.
 DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . .; IDA.
 DR GO; GO:0005515; F:protein binding; IPT.
 DR GO; GO:0007155; P:cell adhesion; IDA.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003598; IG_C2.
 DR InterPro: IPR003585; Neurexin-like.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00294; 4.1m; 1.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 306 AA; 33522 MW; A4CE37B0F2354D5 CRC64;
 Query Match 68.9%; Score 1513.5; DB 11; Length 306;
 Best Local Similarity 95.4%; Pred. No. 4.3e-120;
 Matches 291; Conservative 1; Mismatches 2; Indels 11; Gaps 1;
 QY 130 MIDIQKTAVGEIEVNCCTAMASKPATITRMFKNGKELGKSEVEWSDMTVTTSQML 189
 DB 1 MIDIQKTAVGEIEVNCCTAMASKPATITRMFKNGKELGKSEVEWSDMTVTTSQML 60
 QY 190 KVKHEDGVPIQCVHEPAVTGNLQTORYLEVOYKPOVHIQMTYPLQGLTRGDAPFLTC 249
 DB 61 KVKHEDGVPIQCVHEPAVTGNLQTORYLEVOYKPOVHIQMTYPLQGLTRGDAPFLTC 120
 QY 250 EAIKGPQVWVTWVRVDDEMPQHAVALSGPMLFINNKNKTNGTYRCESNIVGKAHSDYM 309
 DB 121 EAIKGPQVWVTWVRVDDEMPQHAVALSGPMLFINNKNKTNGTYRCESNIVGKAHSDYM 180
 QY 310 LYVVDPTTTPPTTTTTTTTTTTTTTTTTTTTTTTTTTDSRAGEEGTIGAVDHAIV 358
 DB 181 LYVVDPTTTPPTTTTTTTTTTTTTTTTTTTTTTTTTTDSRAGEEGTIGAVDHAIV 240
 QY 359 IGVAVAVVFMCLLITLGRYFAHKGTYFTHAKGADDAADDTALINAGGONNSE 418
 DB 241 IGVAVAVVFMCLLITLGRYFAHKGTYFTHAKGADDAADDTALINAGGONNSE 300
 QY 419 KKEYF 423
 DB 301 KKEYF 305
 RESULT 12
 QOXYL6 PRELIMINARY; PRT; 295 AA.
 AC QOXYL6;
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, last annotation update)
 DE Adhesion protein RA175A.
 GN IGSF4 OR RA175A.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RX [1]
 RN SEQUENCE FROM N.A.
 RA Soyama A., Fujita E., Urabe K., Mukasa T., Kourouku Y., Momoi M.,
 Momoi T.;
 RT "RA175, a novel neuron specific adhesion protein.",
 RL Submitted (Dec-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB021964; BAA87914.1; -
 DR MGD; MGI:1889272; Igsf4.
 DR GO; GO:0045202; C:synaptic junction; IDA.
 DR GO; GO:0008021; C:synaptic vesicle; IDA.
 DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . .; IDA.

DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0007155; P:cell adhesion; IDA.
 DR GO; GO:0007416; P:synaptogenesis; IDA.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_c2.
 DR InterPro; IPR003585; Neurexin-like.
 DR Pfam; PF00047; IG; 2.
 DR SMART; SM00294; 4.1m; 1.
 DR SMART; SM00408; IGc2; 1.
 DR PROSITE; PSS0835; IG-LIKE; 2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 295 AA; 32347 MW; FDD9B8145C6B971B CRC64;

Query Match 68.0%; Score 1493; DB 11; Length 295;
 Best Local Similarity 96.6%; Pred. No. 2,3e-118;
 Matches 284; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 130 MIDIQDVAEGEIEVNCTAMASKPATIRPFKNKELKGSVEEWSDMYTVTSQML 189
 DB 1 MIDIQDVAEGEIEVNCTAMASKPATIRPFKNKELKGSVEEWSDMYTVTSQML 60
 QY 190 KVHKEDDGVPIQVYEHPAVGNLQTORYLEVQYKPOVHQMITYPLQGLTRGDAFELTC 249
 DB 61 KVHKEDDGVPIQVYEHPAVGNLQTORYLEVQYKPOVHQMITYPLQGLTRGDAFELTC 120
 QY 250 EAIGKQPVMVTVWRVDEMPQHAVLSGNLFINNLTNDGTYCEASNIYGAHSDYM 309
 DB 121 EAIGKQPVMVTVWRVDEMPQHAVLSGNLFINNLTNDGTYCEASNIYGAHSDYM 180
 QY 310 LVYVDPTTIPPTTTTTTTTTTTTTTTTTTTTTITDSRAGEEGTGAVDHAYIGVAVVFA 369
 DB 181 LVYVDPTTIPPTTTTTTTTTTTTTTTTTTTTTATTEPAVDSRAGEEGTGAVDHAYIGVAVVFA 240
 QY 370 MCLLIILIGRYFARHKGTYFTHAKGADDAADADTAIINAGGQNNSEKKEYF 423
 DB 241 MCLLIILIGRYFARHKGTYFTHAKGADDAADADTAIINAGGQNNSEKKEYF 294

RESULT 13

Q9QYL5 PRELIMINARY; FRT; 289 AA.

ID Q9QYL5
 AC Q9QYL5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Adhesion protein RAI175B.
 GN IGSF4 OR RAI175B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Soyama A., Fujita E., Urabe K., Mukasa T., Kourouku Y., Momoi M.,
 RA Momoi T.;
 RT Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AB021965; BAA87915.1; -.
 DR MGD; MGI:1889272; Igsf4.
 DR GO; GO:0045202; C:synaptic junction; IDA.
 DR GO; GO:0008021; C:synaptic vesicle; IDA.
 DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . .; IDA.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0007155; P:cell adhesion; IDA.
 DR GO; GO:0007416; P:synaptogenesis; IDA.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_c2.
 DR InterPro; IPR003585; Neurexin-like.
 DR Pfam; PF00047; IG; 2.
 DR SMART; SM00294; 4.1m; 1.
 DR SMART; SM00408; IGc2; 1.
 DR PROSITE; PSS0835; IG-LIKE; 2.
 KW Immunoglobulin domain.

SQ SEQUENCE 289 AA; 31811 MW; 8D1B836D0565AE4 CRC64;

Query Match 63.9%; Score 1404; DB 11; Length 289;
 Best Local Similarity 92.5%; Pred. No. 7.9e-111;
 Matches 272; Conservative 2; Mismatches 14; Indels 6; Gaps 1;

QY 130 MIDIQDVAEGEIEVNCTAMASKPATIRPFKNKELKGSVEEWSDMYTVTSQML 189
 DB 1 MIDIQDVAEGEIEVNCTAMASKPATIRPFKNKELKGSVEEWSDMYTVTSQML 60
 QY 190 KVHKEDDGVPIQVYEHPAVGNLQTORYLEVQYKPOVHQMITYPLQGLTRGDAFELTC 249
 DB 61 KVHKEDDGVPIQVYEHPAVGNLQTORYLEVQYKPOVHQMITYPLQGLTRGDAFELTC 120
 QY 250 EAIGKQPVMVTVWRVDEMPQHAVLSGNLFINNLTNDGTYCEASNIYGAHSDYM 309
 DB 121 EAIGKQPVMVTVWRVDEMPQHAVLSGNLFINNLTNDGTYCEASNIYGAHSDYM 180
 QY 310 LVYVDPTTIPPTTTTTTTTTTTTTTTTTTTTTITDSRAGEEGTGAVDHAYIGVAVVFA 369
 DB 181 LVYVDPTTIPPTTTTTTTTTTTTTTTTTTTTTATTEPAVDSRAGEEGTGAVDHAYIGVAVVFA 234
 QY 370 MCLLIILIGRYFARHKGTYFTHAKGADDAADADTAIINAGGQNNSEKKEYF 423
 DB 235 MCLLIILIGRYFARHKGTYFTHAKGADDAADADTAIINAGGQNNSEKKEYF 288

RESULT 14

Q9QYL3 PRELIMINARY; FRT; 278 AA.

ID Q9QYL3
 AC Q9QYL3;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Adhesion protein RAI175N.
 GN IGSF4 OR RAI175N.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Soyama A., Fujita E., Urabe K., Mukasa T., Kourouku Y., Momoi M.,
 RA Momoi T.;
 RT Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AB021967; BAA87917.1; -.
 DR MGD; MGI:1889272; Igsf4.
 DR GO; GO:0045202; C:synaptic junction; IDA.
 DR GO; GO:0008021; C:synaptic vesicle; IDA.
 DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . .; IDA.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0007155; P:cell adhesion; IDA.
 DR GO; GO:0007416; P:synaptogenesis; IDA.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003585; Neurexin-like.
 DR InterPro; IPR003598; IG_c2.
 DR Pfam; PF00047; IG; 2.
 DR SMART; SM00294; 4.1m; 1.
 DR SMART; SM00408; IGc2; 1.
 DR PROSITE; PSS0835; IG-LIKE; 2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 278 AA; A295F4DEA2724B04 CRC64;

Query Match 62.8%; Score 1380.5; DB 11; Length 278;
 Best Local Similarity 90.8%; Pred. No. 7.4e-109;
 Matches 267; Conservative 2; Mismatches 8; Indels 17; Gaps 1;

QY 130 MIDIQDVAEGEIEVNCTAMASKPATIRPFKNKELKGSVEEWSDMYTVTSQML 189
 DB 1 MIDIQDVAEGEIEVNCTAMASKPATIRPFKNKELKGSVEEWSDMYTVTSQML 60
 QY 190 KVHKEDDGVPIQVYEHPAVGNLQTORYLEVQYKPOVHQMITYPLQGLTRGDAFELTC 249

Db	61	KHKEDDDGVAVICQVHEPRAVIGNLQYRLEQVYKQYHIGMTYPIQSLRREGSALELTC	120
Qy	250	EAIGKPPQVWATYVAVRDDEMPQAVLSCGNLFINTLNTDNGYTRCEASNIYGAHSDYM	309
Db	121	EAIKPPQVWATVAVRDDEMPQAVLSCGNLFINTLNTDNGYTRCEASNIYGAHSDYI	180
Qy	310	LYVYDPTPTIPETTTTTTTTTTTTTLIIITDSRAGEEGTIGAVDAVIGVAAVVFA	369
Db	181	LYVYD-----TTATTEPAVHDSRAGEEGTIGAVDAVIGVAAVVFA	223
Qy	370	MLCIIILIGRPARHKGYETHEAKAGADPAADPAIINAAAGGQNNSEKKEYF	423
Db	224	MLCIIILIGRPARHKGYETHEAKAGADPAADPAIINAAAGGQNNSEKKEYF	277

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QY      350  TIGANDHAYIGVAVVNVVPMCLIIIGRYFAHKKGYFTHFAKGDADDAADATATINA 409
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      365  P-----DHAIIGVAVVAVVTLLCSIFLGRYLARRHKGTYLTNEAKGADPADATATINA 420
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY      410  EGGQNNSEKKEXYF 423
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      421  EGGQVNAEKKEXYF 434
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Search completed: July 7, 2004, 06:02:45
Job time : 60.1711 secs

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RESULT	15			
Q8N3J6				
ID	Q8N3J6	PRELIMINARY;	PRT;	435 AA.
AC	Q8N3J6			
DT	01-OCT-2002 (TrEMBLrel. 22, Created)			
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
DE	Hypotheetical protein.			
GN	DKFZP761G128.			
OS	Homio sapiens (Human).			
OC	Eumaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Hom.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Amygdala;			
RA	Koehler K., Beyer A., Mewes H.W., Weil B., Wiemann S.;			
RL	Submitted (JUL-2002) to the EMBL/Genbank/DDbJ databases.			
DR	EMBL, ALB84270, C3938945.1, ..			
DR	InterPro, IPR003599; IG.			
DR	InterPro, IPR007110, IG-like.			
DR	InterPro, IPR003598; IG_c2.			
DR	Pfam, PF00047; IG; 3.			
DR	SMART, SM00409; IG; 2.			
DR	SMART, SM00408; IGC2; 2.			
DR	PROSITE, PS50835; IG_LIKE; 3.			
DR	Hypotheetical protein; Immunoglobulin domain.			
SQ	SEQUENCE 435 AA; 47554 MW; 59DD41B7F34D46 CRC64;			

Query Match	40.8%;	Score 897;	DB 4;	Length 435;
Best Local Similarity	44.2%;	Pred. No. 1.5e-67;		
Matches 192;	Conservative	75;	Mismatches 139;	Indels 28;
				Gaps 7;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 7, 2004, 05:56:13 / Search time 74.3306 Seconds
(without alignments)
1607.918 Million cell updates/sec

Title: US-10-622-237-4
Perfect score: 2197
Sequence: 1 AAPPGJRLRLILLLSAAL.....TAIINAGGONNSEKKEYF 423

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2197	100.0	423	3	AAAY5093
2	2169	98.7	442	3	ABAB25619
3	2169	98.7	442	3	AAAY94341
4	2169	98.7	442	3	AAAY5092
5	2169	98.7	442	5	AAEL19887
6	2169	98.7	442	5	ABP62825
7	2169	98.7	442	6	ADAE21144
8	2169	98.7	442	7	ADAE54238
9	2169	98.7	442	8	ADAE65825
10	2169	98.6	442	6	ABO07196
11	2166	98.6	442	6	ABO07231
12	2166	98.6	442	7	ADAE61605
13	2166	98.6	442	7	ADAE61608
14	2149	97.8	440	2	AAAY17830
15	2149	97.8	440	3	AAAB1321
16	2149	97.8	440	4	AAU29040
17	2149	97.8	440	6	ABU58415
18	2149	97.8	440	6	ABU87964
19	2149	97.8	440	6	ABU84279
20	2149	97.8	440	6	ABR66153
21	2149	97.8	440	6	ABR65543
22	2149	97.8	440	6	ABU99483
23	2149	97.8	440	6	ABU55930
24	2149	97.8	440	6	ABU87722
25	2149	97.8	440	6	ABU89843

26	2149	97.8	440	6	ABR68092	ABR68092 Human sec
27	2149	97.8	440	6	ABU96145	ABU96145 Novel hum
28	2149	97.8	440	6	ABU92576	ABU92576 Human sec
29	2149	97.8	440	6	ABO08653	ABO08653 Human sec
30	2149	97.8	440	6	ABO02705	ABO02705 Human sec
31	2149	97.8	440	6	ABR74859	ABR74859 Human sec
32	2149	97.8	440	6	ABR94621	ABR94621 Human sec
33	2149	97.8	440	6	ABU60240	ABU60240 Human PRO
34	2149	97.8	440	6	ABU85594	ABU85594 Human PRO
35	2149	97.8	440	6	ABU98754	ABU98754 Novel hum
36	2149	97.8	440	6	ABU97969	ABU97969 Novel hum
37	2149	97.8	440	6	ABU91675	ABU91675 Novel hum
38	2149	97.8	440	6	ABU89368	ABU89368 Human PRO
39	2149	97.8	440	6	ABU86209	ABU86209 Human sec
40	2149	97.8	440	6	ABU67422	ABU67422 Human sec
41	2149	97.8	440	6	ABU80450	ABU80450 Human PRO
42	2149	97.8	440	6	ABR99368	ABR99368 Human PRO
43	2149	97.8	440	6	ABR98758	ABR98758 Human sec
44	2149	97.8	440	6	ABO16281	ABO16281 Human sec
45	2149	97.8	440	6	ABR92181	ABR92181 Human sec

ALIGNMENTS

RESULT 1	AAAY5093	AAAY5093 standard; protein; 423 AA.
XX	XX	XX
AC	AAAY5093;	
XX	XX	XX
DT	31-MAY-2000 (first entry)	
XX	XX	XX
DE	Mouse lymphoid derived dendritic cell adhesion molecule.	
XX	XX	XX
KW	Lymphoid derived dendritic cell adhesion molecule; LDCAM; mouse; B7-1;	
KW	B7-1; T cell proliferation; natural killer cell; NK; tumour cell;	
KW	biological activity; quality control reagent; treatment; inflammation;	
KW	immune system disorder; autoimmune; viral infection; infectious disease;	
XX	organ transplant rejection; bone marrow; modulator; immune response.	
XX	XX	XX
OS	Mus sp.	
XX	XX	XX
FH	Key	Location/Qualifiers
FT	Domain	1..356
FT	Modified-site	/label= Extracellular_domain
FT	Modified-site	/note= "N-Glycosylation site"
FT	Modified-site	83..85
FT	Modified-site	/note= "N-Glycosylation site"
FT	Modified-site	95..97
FT	Modified-site	/note= "N-Glycosylation site"
FT	Modified-site	147..149
FT	Modified-site	/note= "N-Glycosylation site"
FT	Modified-site	286..288
FT	Modified-site	/note= "N-Glycosylation site"
FT	Modified-site	290..292
FT	Modified-site	/note= "N-Glycosylation site"
FT	Domain	357..377
FT	Domain	/label= Transmembrane_domain
FT	Domain	378..423
FT	Domain	/label= Cytoplasmic_domain
PN	MO200008158-A2.	
PD	17-FEB-2000.	
XX	XX	XX
PF	05-AUG-1999;	99WO-US017905.
XX	XX	XX
PR	07-AUG-1998;	98US-0095672P.
XX	XX	XX
PA	(IMMV) IMMUNEX CORP.	
XX	XX	XX

QY	121	TVLVPNNLMIDLOKTA	NAVGEIEIVNCTAMASKPA	TTTRMPKNGKTELKSGSEVEMSDM	180
QY	121 <td>TVLVPNNLMIDLOKTA<td>NAVGEIEIVNCTAMASKPA<td>TTTRMPKNGKTELKSGSEVEMSDM<td>180</td></td></td></td>	TVLVPNNLMIDLOKTA <td>NAVGEIEIVNCTAMASKPA<td>TTTRMPKNGKTELKSGSEVEMSDM<td>180</td></td></td>	NAVGEIEIVNCTAMASKPA <td>TTTRMPKNGKTELKSGSEVEMSDM<td>180</td></td>	TTTRMPKNGKTELKSGSEVEMSDM <td>180</td>	180
Db	139	TVLVPNNLMIDLOKTA <td>NAVGEIEIVNCTAMASKPA<td>TTTRMPKNGKTELKSGSEVEMSDM<td>198</td></td></td>	NAVGEIEIVNCTAMASKPA <td>TTTRMPKNGKTELKSGSEVEMSDM<td>198</td></td>	TTTRMPKNGKTELKSGSEVEMSDM <td>198</td>	198
QY	181	YTVTSQMLKVNKHEDGVPV	COVEHPAVTGNLQTORYLEVQYKPOVHIQMTPELQGLTR		240
Db	199	YTVTSQMLKVNKHEDGVPV	COVEHPAVTGNLQTORYLEVQYKPOVHIQMTPELQGLTR		258
QY	241	EGDAFELTCAICKPOVW	TVWRVDEMPQHAVISGNPLFNNNKTDNCTVCEASNI		300
Db	259	EGDAFELTCAICKPOVW	TVWRVDEMPQHAVISGNPLFNNNKTDNCTVCEASNI		318
QY	301	VGRASDYMLVYVDEPTTIP	PTTTTTTTTTTTTTTTTTTTTTTTTTTTIDSRAGEGTTGADVHAVIG		360
Db	319	VGRASDYMLVYVDEPTTIP	PTTTTTTTTTTTTTTTTTTTTTTTTTTTIDSRAGEGGSIRADVHAVIG		378
QY	361	GVYAVVVFAMLCIIITLGR	YFPAHKQTYTTHAKGADDAADDTAIIIVABEGGNNSEKK		420
Db	379	GVYAVVVFAMLCIIITLGR	YFPAHKQTYTTHAKGADDAADDTAIIIVABEGGNNSEKK		438
QY	421	EYF	423		
Db	439	EYF	441		
RESULT 3					
AA994341	standard; protein; 442 AA.				
AA994341					
AA994341					
XX	AC				
XX	DT	22-AUG-2000 (first entry)			
XX	DE	Human cell surface receptor protein #8.			
XX	XX				
KW	Human; HCSRFP; cytostatic; antiarthritic; antiinflammatory; antirheumatic; immunosuppressive; antidiabetic; sclerotic; antibacterial; antiparasitic; neuroprotective; nootropic; anticomvulsant; cancer; leukemia; melanoma; Alzheimer's diseases; multiple sclerosis; epilepsy.				
OS	Homo sapiens.				
XX	XX				
FT	Key	Location/Qualifiers			
FT	Peptide	1..44			
FT	Protein	/label= Signal_peptide			
FT	Region	45..442			
FT	Region	/label= HCSRFP-6			
FT	Region	53			
FT	Domain	/note= "potential phosphorylation site"			
FT	Region	57..126			
FT	Region	/label= Immunoglobulin_domain			
FT	Region	67			
FT	Region	/note= "potential glycosylation site"			
FT	Region	101			
FT	Region	/note= "potential glycosylation site"			
FT	Region	103			
FT	Region	/note= "potential phosphorylation site"			
FT	Region	113			
FT	Region	/note= "potential glycosylation site"			
FT	Region	115			
FT	Region	/note= "potential phosphorylation site"			
FT	Region	155			
FT	Domain	/note= "potential phosphorylation site"			
FT	Region	159..222			
FT	Region	/label= Immunoglobulin_domain			
FT	Region	165			
FT	Region	/note= "potential glycosylation site"			
FT	Region	176			
FT	Region	/note= "potential phosphorylation site"			
FT	Region	190			
FT	Region	/note= "potential phosphorylation site"			
FT	Region	233			

Query Match	Best Local Similarity	Score	DB	Length	Matches	Conservative	Mismatches	Indels	Gaps
1	98.7%	2169	3	442	418	1	4	0	0
<p>Sequence 442 AA;</p> <p>Sequence 442 AA;</p> <p>Query Match</p> <p>Best Local Similarity 98.7%;</p> <p>Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0</p>									

```

QY 61 PNRQTIYFRDPRPLKDSRFQILNFSSELKVSITNVSISDEGRYFCQLYTDPQESYTTI 120
DB 79 PNRQTIYFRDPRPLKDSRFQILNFSSELKVSITNVSISDEGRYFCQLYTDPQESYTTI 138
QY 121 TVVPPRNLMIDIOKOTAVEGEIEVNCJAMASKPATIIRWFKNGKELKSKSEVEWSDM 180
DB 139 TVVPPRNLMIDIOKOTAVEGEIEVNCJAMASKPATIIRWFKNGKELKSKSEVEWSDM 198
QY 181 YTVTSQMLKVKHKEDDGVPIQVEHPAVTGNLQTORYLEVOYKPOVHIQMTYPLQGLTR 240
DB 199 YTVTSQMLKVKHKEDDGVPIQVEHPAVTGNLQTORYLEVOYKPOVHIQMTYPLQGLTR 258
QY 241 EGDAPFELTCEAIGKPOPVMTWVRVDEMPQHAULSGPNLFINNLTNDNGTRCEASNI 300
DB 259 EGDAPFELTCEAIGKPOPVMTWVRVDEMPQHAULSGPNLFINNLTNDNGTRCEASNI 318
QY 301 VGKASDYMVLVYDPPPTIIPPTTTTTTTTTTTTTTTTTTTTTDSRAGEEGTIGAVDHAIVG 360
DB 319 VGKASDYMVLVYDPPPTIIPPTTTTTTTTTTTTTTTTTTTTTDSRAGEEGSIRAVDHAIVG 378
QY 361 GVAAVVVFAMLCILIIIGRYFARHKGYFTHEAKGADDAADADTAIINAGGQNNSEKK 420
DB 379 GVAAVVVFAMLCILIIIGRYFARHKGYFTHEAKGADDAADADTAIINAGGQNNSEKK 438
QY 421 EYF 423
DB 439 EYF 441

RESULT 4
AAV45092
ID AAV45092 standard; protein; 442 AA.
AC AAV45092;
XX
XX 31-MAY-2000 (first entry)
DE Human lymphoid derived dendritic cell adhesion molecule.
XX
XX Lymphoid derived dendritic cell adhesion molecule; LDCAM; human; B7-1;
KM B7-1; T cell proliferation; natural killer cell; NK; tumour cell;
KM biological activity; quality control reagent; treatment; inflammation;
KM immune system disorder; autoimmune; viral infection; infectious disease;
KM organ transplant rejection; bone marrow; modulator; immune response.
XX
XX Homo sapiens.
OS
XX Location/Qualifiers
XX Key 1..374
XX Domain /label= Extracellular_domain
XX Peptide 1..38
XX Protein /label= Leader_peptide
XX Modified-site 39..442
XX /label= Mature_human_LDCAM_polypeptide
XX /note= 67..69
XX /note= "N-Glycosylation site"
XX /note= 101..103
XX /note= "N-Glycosylation site"
XX /note= 113..115
XX /note= "N-Glycosylation site"
XX /note= 165..167
XX /note= "N-Glycosylation site"
XX /note= 304..306
XX /note= "N-Glycosylation site"
XX /note= 308..310
XX /note= "N-Glycosylation site"
XX /note= 375..395
XX /label= Transmembrane_domain
XX /label= 396..442
XX /label= Cytoplasmic_domain
XX
XX WO200008158-A2.

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XX 17-FEB-2000.
XX
XX 05-AUG-1999; 99MO-US017505.
XX
XX 07-AUG-1998; 98US-0095672P.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Baum PR, Fanslow WC;
XX
XX WPI: 2000-205712/18.
XX
XX N-PSDB; AA250882.
XX
XX Novel molecules designated LDCAM are capable of altering or modulating T
XX cell function.
XX
XX Claim 7; Page 42-43; 44pp; English.
XX
XX The present amino acid sequence is the human lymphoid derived dendritic
XX cell adhesion molecule, LDCAM. It is found on lymphoid derived dendritic
XX cells and displays homology to adhesion molecules, B7-1 and cytoplasmic
XX region of B7-1. Human LDCAM is expressed in breast, retina, foetal
XX liver, spleen and heart, lung, muscle, placenta, thymoid and lung
XX carcinoma. LDCAM polypeptides interact with T cell surface molecules to
XX alter signalling and inhibits T cell proliferation, bind to themselves
XX and B7-1; an LDCAM binding protein and increases natural killer (NK)
XX cell populations. It may be used to measure the biological activity and
XX as quality control reagents of LDCAM binding proteins. LDCAM may be used
XX for treating disorders associated with malfunctioning of immune system,
XX inflammation, autoimmune disorders, viral infected cells, infectious
XX diseases and for killing tumour cells. They are also useful for
XX prevention or reducing the effect of organ and bone marrow transplant
XX rejection and for modulating T cell immune response. LDCAM polypeptides
XX may also be used as carriers for delivering agents attached to T cells or
XX cells bearing B7-1
XX
XX Sequence 442 AA:
XX
XX Query Match 98.7%; Score 2169; DB 3; Length 442;
XX Best Local Similarity 98.8%; Pred. No. 2.1e-149;
XX Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
XX
XX 1 AAPGLRLRLILLLLSAAALIPITGQNLFTKDYTVIEGVATISQVNSDSDSVIQLN 60
XX 19 AAPGLRLRLILLLLSAAALIPITGQNLFTKDYTVIEGVATISQVNSDSDSVIQLN 78
XX
XX 61 PNRQTIYFRDPRPLKDSRFQILNFSSELKVSITNVSISDEGRYFCQLYTDPQESYTTI 120
XX 79 PNRQTIYFRDPRPLKDSRFQILNFSSELKVSITNVSISDEGRYFCQLYTDPQESYTTI 138
XX
XX 121 TVVPPRNLMIDIOKOTAVEGEIEVNCJAMASKPATIIRWFKNGKELKSKSEVEWSDM 180
XX 139 TVVPPRNLMIDIOKOTAVEGEIEVNCJAMASKPATIIRWFKNGKELKSKSEVEWSDM 198
XX
XX 181 YTVTSQMLKVKHKEDDGVPIQVEHPAVTGNLQTORYLEVOYKPOVHIQMTYPLQGLTR 240
XX 199 YTVTSQMLKVKHKEDDGVPIQVEHPAVTGNLQTORYLEVOYKPOVHIQMTYPLQGLTR 258
XX
XX 241 EGDAPFELTCEAIGKPOPVMTWVRVDEMPQHAULSGPNLFINNLTNDNGTRCEASNI 300
XX 259 EGDAPFELTCEAIGKPOPVMTWVRVDEMPQHAULSGPNLFINNLTNDNGTRCEASNI 318
XX
XX 301 VGKASDYMVLVYDPPPTIIPPTTTTTTTTTTTTTTTTTTTTTDSRAGEEGTIGAVDHAIVG 360
XX 319 VGKASDYMVLVYDPPPTIIPPTTTTTTTTTTTTTTTTTTTTTDSRAGEEGSIRAVDHAIVG 378
XX
XX 361 GVAAVVVFAMLCILIIIGRYFARHKGYFTHEAKGADDAADADTAIINAGGQNNSEKK 420
XX 379 GVAAVVVFAMLCILIIIGRYFARHKGYFTHEAKGADDAADADTAIINAGGQNNSEKK 438
XX
XX 421 EYF 423
XX
XX

```


CC sclerosis), immune deficiencies, cancer, autoimmune disorders, multiple
 CC sclerosis, diabetes and allergies. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 442 AA:

Query Match 98.7%; Score 2169; DB 5; Length 442;
 Best Local Similarity 98.8%; Pred. No. 2.1e-149;
 Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPGRLRLRLLLLSAAALIPFGDGNLFKQDVTVEGEVATISGVNKSDDSVIQLN 60
 DB 19 AAPGRLRLRLLLLSAAALIPFGDGNLFKQDVTVEGEVATISGVNKSDDSVIQLN 78
 QY 61 PNRQTIYFRDPRPLKDSRFQNLNFSSELKSLTNVSIISDEGRYFCQLYTDPQESYTTI 120
 DB 79 PNRQTIYFRDPRPLKDSRFQNLNFSSELKSLTNVSIISDEGRYFCQLYTDPQESYTTI 138
 QY 121 TVLVPPRNLMIDIQKDTAVGESEIENVCTAMASKPATITRMFKGNELKSGSEVEEWSM 180
 DB 139 TVLVPPRNLMIDIQKDTAVGESEIENVCTAMASKPATITRMFKGNELKSGSEVEEWSM 198
 QY 181 YVTSQMLKVKHEDDGVPICOVEHPAVTGNLQTORYLEVOYKPOVHIQMTYPLQGLTR 240
 DB 199 YVTSQMLKVKHEDDGVPICOVEHPAVTGNLQTORYLEVOYKPOVHIQMTYPLQGLTR 258
 QY 241 EGDAPETGALGKPPQVNTWTRVDDENPOHNVLSGPNLFNNLKTNGTYRCASNI 300
 DB 259 EGDAPETGALGKPPQVNTWTRVDDENPOHNVLSGPNLFNNLKTNGTYRCASNI 318
 QY 301 VGNKSDYMLVYVDPPTTITPTTTTTTTTTTTTTTTTTTTTTTTTTTTSDRAGEEGTIGAVDAVIG 360
 DB 319 VGNKSDYMLVYVDPPTTITPTTTTTTTTTTTTTTTTTTTTTTTTTTTSDRAGEEGTIGAVDAVIG 378
 QY 361 GVAVAVVFAMLCIIILIGRYFAHKGTYFTEHAKGADDAADTAIINAGGONNSEKK 420
 DB 379 GVAVAVVFAMLCIIILIGRYFAHKGTYFTEHAKGADDAADTAIINAGGONNSEKK 438
 QY 421 EYF 423
 DB 439 EYF 441

RESULT 7
 ADA27144
 ID ADA27144 standard; protein: 442 AA.
 AC ADA27144;
 DT 20-NOV-2003 (first entry)
 XX 20-NOV-2003 (first entry)
 DE Human novel secreted protein from gene 11 #3.
 XX
 KM cytosolic; antiinflammatory; immunomodulator; neuroprotective;
 KM hemostatic; gene therapy; cancer; inflammation; immune disorder;
 KM neurological disorder; blood clotting disorder; food additive;
 KM preservative; human; secreted protein.
 XX
 OS Homo sapiens.
 XX
 PN US2003055231-A1.
 XX 20-MAR-2003.
 XX 29-OCT-2001; 2001US-00984130.
 XX 28-OCT-1998; 98US-0105971P.
 XX 27-OCT-1999; 99MO-US025031.
 XX 19-APR-2000; 2000US-0198407P.
 XX 30-OCT-2000; 2000US-0243792P.
 XX 18-APR-2001; 2001US-00836353.

XX (NIJ/J) NI J.
 PA (YOUNG) YOUNG P E.
 PA (KENN) KENNY J J.
 PA (OLSE) OLSEN H S.
 PA (MOOR) MOORE P A.
 PA (WEI) WEI Y.
 PA (GREEN) GREENE J M.
 PA (RUBEN) RUBEN S M.
 PA (LIU) LIU D.
 PA (CROCK) CROCKER P R.
 PI NI J, Young PE, Kenny JJ, Olsen HS, Moore PA, Wei Y, Greene JM;
 PI Ruben SM, Liu D, Crocker PR;
 PI WPI: 2003-567103/53.

DR New human secreted nucleic acid molecules and polypeptides, useful for
 PT preventing, treating, or ameliorating a medical condition, such as
 PT cancer, inflammation, immune disorders, neurological and blood clotting
 PT disorders.

PS Disclosure; Page 72; 454p; English.

XX The invention relates to an isolated nucleic molecule that is at least
 CC 95% identical to 18 human cDNA sequences representing 12 novel genes
 CC encoding secreted proteins or a polynucleotide fragment of the cDNA
 CC sequence contained in American Type Culture Collection (ATCC) deposit No.
 CC defined in the specification, its species homologue, a variant or allelic
 CC variant of the polynucleotide having a polynucleotide capable of
 CC hybridizing under stringent conditions to a nucleic acid molecule
 CC does not hybridize under stringent conditions to a nucleic acid molecule
 CC having a nucleotide sequence of only A or T residues. Also included are
 CC recombinant vectors, host cells (for producing the polypeptide), the
 CC secreted polypeptide (comprising a sequence that is at least 95%
 CC identical to a polypeptide fragment, domain, epitope, full-length
 CC protein, variant, allelic variant or species homologue), antibodies that
 CC specifically bind to the polypeptides, diagnosing, treating, preventing
 CC or ameliorating a medical condition by administering the polynucleotide
 CC or the polypeptide, the gene corresponding to the cDNA sequence and
 CC identifying an activity in a biological assay (by expressing the cDNA
 CC sequence in a cell, isolating the supernatant, and detecting an activity
 CC in a biological assay and identifying the protein in the supernatant
 CC having the activity). The polypeptides, nucleic acids and antibodies are
 CC useful for diagnosing a pathological condition or a susceptibility to a
 CC pathological condition, for preventing, treating, or ameliorating a
 CC medical condition, such as cancer, inflammation and other immune
 CC disorders, neurological and blood clotting disorders (many examples are
 CC given in the specification). The nucleic acids are also useful for
 CC chromosome identification, radiation hybrid mapping or long-range
 CC restriction mapping. The polypeptides and antibodies are useful for
 CC providing immunological probes for differential identification of the
 CC tissues immunohistochemistry assays. The polypeptide, polynucleotide,
 CC agonist or antagonist may also be used as a food additive or preservative
 CC to increase or decrease storage capabilities, fat content or other
 CC nutritional components. The present is a secreted protein of the
 CC invention.

XX Sequence 442 AA:

Query Match 98.7%; Score 2169; DB 6; Length 442;
 Best Local Similarity 98.8%; Pred. No. 2.1e-149;
 Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPGRLRLRLLLLSAAALIPFGDGNLFKQDVTVEGEVATISGVNKSDDSVIQLN 60
 DB 19 AAPGRLRLRLLLLSAAALIPFGDGNLFKQDVTVEGEVATISGVNKSDDSVIQLN 78
 QY 61 PNRQTIYFRDPRPLKDSRFQNLNFSSELKSLTNVSIISDEGRYFCQLYTDPQESYTTI 120
 DB 79 PNRQTIYFRDPRPLKDSRFQNLNFSSELKSLTNVSIISDEGRYFCQLYTDPQESYTTI 138
 QY 121 TVLVPPRNLMIDIQKDTAVGESEIENVCTAMASKPATITRMFKGNELKSGSEVEEWSM 180

XX 10-JUL-2003.
 PD 18-APR-2001; 2001US-00836353.
 XX
 PR 28-OCT-1998; 98US-0105971P.
 XX 27-OCT-1999; 99MO-US025031.
 PR 19-APR-2000; 2000US-0198407P.
 XX
 PA (NITJ/) NI J.
 PA (YOUN/) YOUNG P E.
 PA (KENN/) KENNY J J.
 PA (OLSE/) OLSEN H S.
 PA (MOOR/) MOORE P A.
 PA (WEIY/) WEI Y.
 PA (GREB/) GREENE J M.
 PA (RUBE/) RUBEN S M.
 XX
 PI Nt J, Young PE, Kenny JU, Olsen HS, Moore PA, Wei Y, Greene JM;
 PI Ruben SM;
 XX
 DR WPI; 2004-020335/02.
 XX
 PT New nucleic acid molecule, useful for preparing a medicament for
 PT preventing, treating or ameliorating a medical condition e.g. cancer,
 PT liver disorders or neural disorders.
 XX
 PS Disclosure; SEQ ID NO 136; 380bp; English.
 XX
 CC The invention relates to an isolated nucleic acid sequence, or its
 CC allelic variant, a fragment of the cDNA sequence, or its fragment,
 CC domain, epitope or species homologue. The nucleic acid is useful for
 CC preparing a medicament for preventing, treating or ameliorating a medical
 CC condition e.g., cancer, liver disorders such as hepatitis or neural
 CC disorders such as Alzheimer's disease. The present sequence represents
 CC the amino acid sequence of a novel human secreted protein associated
 CC protein.
 CC
 XX
 SQ Sequence 442 AA;
 Query Match 98.7%; Score 2169; DB 8; Length 442;
 Best Local Similarity 98.8%; Pred. No. 2.1e-149;
 Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

DB 439 EYF 441
 RESULT 10
 ABO07196
 ID ABO07196 standard; protein; 442 AA.
 XX
 AC ABO07196;
 XX
 DT 13-AUG-2003 (first entry)
 XX
 DE Human p53 modifying protein, SEQ ID 156.
 XX
 KW Human; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic;
 KW antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer;
 KW lung cancer; ovarian cancer; angiogenesis; cell cycle;
 KW apoptotic disorder; cell proliferation disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200299122-A1.
 XX
 PD 12-DEC-2002.
 XX
 PF 03-JUN-2002; 2002MO-US017382.
 XX
 PR 05-JUN-2001; 2001US-0296076P.
 PR 10-OCT-2001; 2001US-0328605P.
 PR 15-FEB-2002; 2002US-0357253P.
 XX
 PA (EXEL-) EXELIXIS INC.
 PI Friedman L, Plozman GD, Belvin M, Francis-Liang H, Li D, Funke RP;
 DR N-PSDB; ACD13371.
 XX
 PT Identifying modulators of the p53 pathway for use in treating apoptotic
 PT or cell proliferation disorders, comprises screening for agents that
 PT modulate activity of a human ortholog of genes that modify the p53
 PT pathway in Drosophila.
 PS Example 2; Page 469-470; 678bp; English.
 XX
 CC The invention relates to identifying (M1) a candidate p53 pathway
 CC modulating agent, by contacting an assay system comprising a purified HM
 CC polypeptide (human ortholog of genes that modify the p53 pathway in
 CC Drosophila) or nucleic acid with a test agent under conditions, where but
 CC for the presence of the test agent, the system provides a reference
 CC activity, and detecting a test agent-biased activity of the assay system.
 CC Also included are modulating (M2) a p53 pathway of a cell (comprising
 CC contacting a cell defective in p53 function with a candidate modulator
 CC that specifically binds to a HM polypeptide comprising an HM amino acid
 CC sequence, where p53 function is restored), modulating (M3) a p53 pathway
 CC in a mammalian cell (comprising contacting the cell with an agent that
 CC specifically binds an HM polypeptide or nucleic acid), and diagnosing (M4)
 CC a disease in a patient (comprising: (a) obtaining a biological sample
 CC from the patient; (b) contacting the sample with a probe for HM
 CC expression; (c) comparing the results with a control; and (d) determining
 CC whether the comparison indicates a likelihood disease). (M1) is useful
 CC for identifying modulators of the p53 pathway. A probe for HM expression
 CC is useful for diagnosing breast, colon, kidney, lung and ovarian cancer,
 CC in a patient, where the cancer has greater than 25 % expression level.
 CC Modulators identified by (M1) are useful in a variety of diagnostic and
 CC therapeutic applications, where disease or disorder prognosis is related
 CC to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell
 CC proliferation disorders (e.g. cancer). Another two new methods (M2 and
 CC M3) are useful for modulating the p53 pathway of a cell, thus restoring
 CC the p53 function of the cell, so that the cell undergoes normal
 CC proliferation or progression through the cell cycle. (M2) and (M3) are
 CC also useful for treating defects in the p53 pathway such as angiogenic,
 CC apoptotic or cell proliferation disorders. The present sequence

[illegible]

DR N-PSDB; ACD13404.

XX Identifying modulators of the p53 pathway for use in treating apoptotic

PT or cell proliferation disorders, comprises screening for agents that

PT modulate activity of a human ortholog of genes that modify the p53

PT pathway in *Drosophila*.

XX Example 2; Page 557-559; 678bp; English.

XX The invention relates to identifying (M1) a candidate p53 pathway

CC modulating agent, by contacting an assay system comprising a purified HM

CC polypeptide (human orthologue of genes that modify the p53 pathway in

CC *Drosophila*) or nucleic acid with a test agent under conditions, where but

CC for the presence of the test agent, the system provides a reference

CC activity, and detecting a test agent-biased activity of a cell (comprising

CC Also included are modulating (M2) a p53 pathway of a cell (comprising

CC contacting a cell defective in p53 function with a candidate modulator

CC that specifically binds to a HM polypeptide comprising an HM amino acid

CC sequence, where p53 function is restored), modulating (M3) a p53 pathway

CC in a mammalian cell (comprising contacting the cell with an agent that

CC specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4)

CC a disease in a patient (comprising: (a) obtaining a biological sample

CC from the patient; (b) contacting the sample with a probe for HM

CC expression); (c) comparing the results with a control; and (d) determining

CC whether the comparison indicates a likelihood disease). (M1) is useful

CC for identifying modulators of the p53 pathway. A probe for HM expression

CC is useful for diagnosing breast, colon, kidney, lung and ovarian cancer,

CC in a patient, where the cancer has greater than 25 % expression level.

CC Modulators identified by (M1) are useful in a variety of diagnostic and

CC therapeutic applications, where disease or disorder prognosis is related

CC to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell

CC proliferation disorders (e.g. cancer). Another two new methods (M2 and

CC M3) are useful for modulating the p53 pathway of a cell, thus restoring

CC the p53 function of the cell, so that the cell undergoes normal

CC proliferation or progression through the cell cycle. (M2) and (M3) are

CC also useful for treating defects in the p53 pathway such as angiogenic,

CC apoptotic or cell proliferation disorders. The present sequence

CC represents a human p53 pathway modifying protein

XX

XX Sequence 442 AA;

QY Query Match 98.6%; Score 2166; DB 6; Length 442;

Db Best Local Similarity 98.6%; Pred. No. 3.4e-149;

Matches 417; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPGRLRLRLLLLSAALLPTGDSGNLFTKDVTVIEGEVATISQVYNKSDSDVLTLLN 60

Db 19 AAPGLRLRLRLLLLSAALLPTGDSGNLFTKDVTVIEGEVATISQVYNKSDSDVLTLLN 78

QY 61 PNROTIFRPRPKDSRFOLNNSSEELKVSLTNVSISDEGRFECOLYTDPPDESYYTI 120

Db 79 PNROTIFRPRPKDSRFOLNNSSEELKVSLTNVSISDEGRFECOLYTDPPDESYYTI 138

QY 121 TVLVPNNLMIDIKDTAVVEGEELIVNCTAMASKPATIIRFKKNKELKGSVEEWSDM 180

Db 139 TVLVPNNLMIDIKDTAVVEGEELIVNCTAMASKPATIIRFKKNKELKGSVEEWSDM 198

QY 181 YTVTSOLMLKVKHEDDGPVTCQVEHNAVNGNLTQRYLAEVQKPOVHIQNTYPLQGLTR 240

Db 199 YTVTSOLMLKVKHEDDGPVTCQVEHNAVNGNLTQRYLAEVQKPOVHIQNTYPLQGLTR 258

QY 241 EGDAPFELTCEAIKGRQPVMTWTWVVDDEMPHVALSGPNLEINNLTNDNGTYSCEASNI 300

Db 259 EGDALFELTCEAIKGRQPVMTWTWVVDDEMPHVALSGPNLEINNLTNDNGTYSCEASNI 318

QY 301 VGRKHSYMLVYVDPPTTPTTTTTTTTTTTTTTTTTTSDSAGEGATGAVDHAVIG 360

Db 319 VGRKHSYMLVYVDPPTTPTTTTTTTTTTTTTTTTTTSDSAGEGATGAVDHAVIG 378

QY 361 GVAVVVVFAMLCILIIIGRYFAHKGTYFTHEAKGADDAADADATAIINAEGGUNNSEKK 420

Db 379 GVAVVVVFAMLCILIIIGRYFAHKGTYFTHEAKGADDAADADATAIINAEGGUNNSEKK 438

OY 421 EYF 423
|||
Db 439 EYF 441

RESULT 12
ADE61605
ID ADE61605 standard; protein: 442 AA.
AC ADE61605;
XX
XX
DT 29-JAN-2004 (first entry)
XX
XX Human Protein AAF69029, SEQ ID NO 7525.
XX
XX Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
OS Homo sapiens.
XX
XX MO2003016475-A2.
XX
XX PD 27-FEB-2003.
XX
XX PF 14-AUG-2002; 2002MO-US025765.
XX
XX PR 14-AUG-2001; 2001US-0312147P.
XX
XX PR 01-NOV-2001; 2001US-0346382P.
XX
XX PR 26-NOV-2001; 2001US-0333347P.
XX
XX PA (GENO) GEN HOSPITAL CORP.
XX
XX PA (FARB) BAYER AG.
XX
XX PI Woolf C, D'urso D, Befort K, Costigan M;
XX
XX WPI; 2003-268312/26.
XX
XX DR GENBANK; AAF69029.
XX
XX PT New composition comprising two or more isolated polypeptides, useful for
XX
XX PT preparing a medicament for treating pain in an animal.
XX
XX PS Claim 1; Page; 1017P; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
XX
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX
XX derivative or allelic variation of the nucleic acid sequence. Also
XX
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX
XX comprising the vector, a method for identifying a nucleotide sequence
XX
XX which is differentially regulated in an animal subjected to pain and a
XX
XX kit to perform the method, an array, a method for identifying an agent
XX
XX that increases or decreases the expression of the polynucleotide sequence
XX
XX that is differentially expressed in neuronal tissue of a first animal
XX
XX subjected to pain, a method for identifying a compound which regulates
XX
XX the expression of a polynucleotide sequence which is differentially
XX
XX expressed in an animal subjected to pain, a method for identifying a
XX
XX compound that regulates the activity of one or more of the
XX
XX polynucleotides, a method for producing a pharmaceutical composition, a
XX
XX method for identifying a compound or small molecule that regulates the
XX
XX activity in an animal of one or more of the polypeptides given in the
XX
XX specification, a method for identifying a compound useful in treating
XX
XX pain and a pharmaceutical composition comprising the one or more
XX
XX polypeptides or their antibodies. The polynucleotide and the compound that
XX
XX modulates its activity is useful for preparing a medicament for treating
XX
XX pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
XX
XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
XX
XX therapy). The sequence presented is a human protein (shown in Table 2 of
XX
XX the specification) which is differentially expressed during pain. Note:
XX
XX The sequence data for this patent did not form part of the printed
XX
XX specification, but was obtained in electronic form directly from WPI at
XX
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 442 AA:
SO

Query Match 98.6%; Score 2166; DB 7; Length 442;
Best Local Similarity 98.6%; Pred. No. 3,4e-149;
Matches 417; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 AAPPGLRLRLILLLLSAALIPDGQNLPTTKQVTVIEGVATISQVNSDDSVIQLLN 60
Db 19 AAPPGLRLRLILLLLSAALIPDGQNLPTTKQVTVIEGVATISQVNSDDSVIQLLN 78
OY 61 PNROTIFRDPRLPKDSRFCLLNFSSELSKSLTNVSIISDEGRYFCQLYTPDQESYTTI 120
Db 79 PNROTIFRDPRLPKDSRFCLLNFSSELSKSLTNVSIISDEGRYFCQLYTPDQESYTTI 138
OY 121 TLVPPRNLMIDICKDTAVGESEIEVNCITMASKPATTTIMFGKNELKKSVEEWSMD 180
Db 139 TLVPPRNLMIDICKDTAVGESEIEVNCITMASKPATTTIMFGKNELKKSVEEWSMD 198
OY 181 YTVTSQMLKVKHKKDDGVPVICOVEHPAVTGNLQTORYLEVQYKPOVHIQWTYPLQGLTR 240
Db 199 YTVTSQMLKVKHKKDDGVPVICOVEHPAVTGNLQTORYLEVQYKPOVHIQWTYPLQGLTR 258
OY 241 EGDAPFELTCEAIGKRPQVMTWVRVDDDEMPQHAVLSGPNLFINNLTNDGTRCEASNI 300
Db 259 EGDALFELTCEAIGKRPQVMTWVRVDDDEMPQHAVLSGPNLFINNLTNDGTRCEASNI 318
OY 301 VGKASDMLVYVPPPTTPTTTTPTTTTPTTTTPTTTTPTTTTPTTTTPTTTTPTTTTPTTT 360
Db 319 VGKASDMLVYVPPPTTPTTTTPTTTTPTTTTPTTTTPTTTTPTTTTPTTTTPTTTTPTTT 378
OY 361 GVVAVVVFAMLCIIIIIGRYFARHKGTFTHEAKGADDAADATAIINAEQGNSEKK 420
Db 379 GVVAVVVFAMLCIIIIIGRYFARHKGTFTHEAKGADDAADATAIINAEQGNSEKK 438
OY 421 EYF 423
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Db 439 EYF 441

RESULT 13
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ID ADE61608 standard; protein: 442 AA.
XX
XX ADE61608;
XX
XX DT 29-JAN-2004 (first entry)
XX
XX DE Human Protein AAF69029, SEQ ID NO 7528.
XX
XX KW Human; pain; neuronal tissue; gene therapy;
XX
XX KW spinal segmental nerve injury; chronic constriction injury; CCI;
XX
XX KW spared nerve injury; SNI; Chung.
XX
XX OS Homo sapiens.
XX
XX PN WO2003016475-A2.
XX
XX PD 27-FEB-2003.
XX
XX PF 14-AUG-2002; 2002MO-US025765.
XX
XX PR 14-AUG-2001; 2001US-0312147P.
XX
XX PR 01-NOV-2001; 2001US-0346382P.
XX
XX PR 26-NOV-2001; 2001US-0333347P.
XX
XX PA (GENO) GEN HOSPITAL CORP.
XX
XX PA (FARB) BAYER AG.
XX
XX PI Woolf C, D'urso D, Befort K, Costigan M;
XX
XX WPI; 2003-268312/26.
XX
XX DR GENBANK; AAF69029.
XX
XX PT New composition comprising two or more isolated polypeptides, useful for

Db	377	GVAVVVFAMLCLLIIIGRYFARHKGTFTHEAKGADDAADDTAIIINAEQNNSEKK	436
Qy	421	EYF 423	
Db	437	EYF 439	

Search completed: July 7, 2004, 05:59:12
Job time : 75.3306 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 7, 2004, 06:02:51, Search time 606.382 Seconds

(without alignments)
217.146 Million cell updates/sec

Title: US-10-622-237-4

Perfect score: 1 AAPGRLRLLLLSAAL.....TALINBGGONNSEEKKEVF 423

Sequence:

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1276540 seqs, 311283616 residues

Total number of hits satisfying chosen parameters: 1276540

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications AA:
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17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2197	100.0	423	9	US-09-778-510-22
2	2197	100.0	423	9	US-09-778-1878-4
3	2197	100.0	423	14	US-10-302-041-22
4	2197	100.0	445	15	US-10-015-115-112
5	2176.5	99.1	449	15	US-10-015-115-113
6	2169	98.7	442	9	US-09-778-510-20
7	2169	98.7	442	9	US-09-778-1878-2
8	2169	98.7	442	10	US-09-884-130-136
9	2169	98.7	442	10	US-09-836-353A-136
10	2169	98.7	442	12	US-10-363-615-262
11	2169	98.7	442	14	US-10-302-041-20
12	2169	98.7	442	14	US-10-403-107-1
13	2169	98.7	442	15	US-10-015-115-111
14	2166	98.6	442	15	US-10-015-115-110
15	2149	97.8	440	9	US-09-866-028-61

16	2149	97.8	440	9	US-09-944-449-61	Sequence 61, Appl
17	2149	97.8	440	9	US-09-944-457-61	Sequence 61, Appl
18	2149	97.8	440	9	US-09-944-462-61	Sequence 61, Appl
19	2149	97.8	440	9	US-09-945-587-61	Sequence 61, Appl
20	2149	97.8	440	9	US-09-945-015-61	Sequence 61, Appl
21	2149	97.8	440	9	US-09-944-396-61	Sequence 61, Appl
22	2149	97.8	440	9	US-09-944-037-61	Sequence 61, Appl
23	2149	97.8	440	9	US-09-944-432-61	Sequence 61, Appl
24	2149	97.8	440	9	US-09-943-762-61	Sequence 61, Appl
25	2149	97.8	440	9	US-09-944-929-61	Sequence 61, Appl
26	2149	97.8	440	9	US-09-943-851A-61	Sequence 61, Appl
27	2149	97.8	440	9	US-09-944-413-61	Sequence 61, Appl
28	2149	97.8	440	9	US-09-944-403-61	Sequence 61, Appl
29	2149	97.8	440	9	US-09-944-896-61	Sequence 61, Appl
30	2149	97.8	440	9	US-09-944-944-61	Sequence 61, Appl
31	2149	97.8	440	9	US-09-944-929-61	Sequence 61, Appl
32	2149	97.8	440	9	US-09-944-907-61	Sequence 61, Appl
33	2149	97.8	440	10	US-09-944-884-61	Sequence 61, Appl
34	2149	97.8	440	10	US-09-944-852-61	Sequence 61, Appl
35	2149	97.8	440	10	US-09-943-780-61	Sequence 61, Appl
36	2149	97.8	440	11	US-09-945-584-61	Sequence 61, Appl
37	2149	97.8	440	12	US-10-206-915-34	Sequence 34, Appl
38	2149	97.8	440	12	US-10-199-670-34	Sequence 34, Appl
39	2149	97.8	440	12	US-10-201-858-34	Sequence 34, Appl
40	2149	97.8	440	12	US-10-205-890-34	Sequence 34, Appl
41	2149	97.8	440	12	US-10-208-024-34	Sequence 34, Appl
42	2149	97.8	440	12	US-10-201-853-34	Sequence 34, Appl
43	2149	97.8	440	12	US-10-677-471-61	Sequence 61, Appl
44	2149	97.8	440	12	US-10-677-669-61	Sequence 61, Appl
45	2149	97.8	440	12	US-10-174-581-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-09-778-510-22
Sequence 22, Application US/09778510
Patent No. US0020164686A1
GENERAL INFORMATION:
APPLICANT: Baum, Peter
TITLE OF INVENTION: Molecules Designated B7L1
FILE REFERENCE: 2844-US
CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: PCT/US99/17906
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: 1998-08-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO: 22
LENGTH: 423
TYPE: PRT
ORGANISM: Mus musculus
US-09-778-510-22

Query Match	100.0%	Score 2197	DB 9	Length 423
Best Local Similarity	100.0%	Pred. No. 1.1e-170		
Matches 423	Conservative	0	Mismatches 0	Indels 0
			Gaps 0	
QY	1	AAPGRLRLLLLSAALITGCGNULFTKCVTVIEGVATISCONKSDSVITQLN	60	
DB	1	AAPGRLRLLLLSAALITGCGNULFTKCVTVIEGVATISCONKSDSVITQLN	60	
QY	61	PRQTIYDFEPLKDSRFQNLNFSSELKSLTNVSISSDEGRYCCQYTPPOBSYTTI	120	
DB	61	PRQTIYDFEPLKDSRFQNLNFSSELKSLTNVSISSDEGRYCCQYTPPOBSYTTI	120	
QY	121	TVLVPPRNIMDIQDTAVEGEIEVNCTAMASKPATIRFKKKEIKGSEVEWSDM	180	
DB	121	TVLVPPRNIMDIQDTAVEGEIEVNCTAMASKPATIRFKKKEIKGSEVEWSDM	180	

QY 181 YTVTSQMLKVKHKEDDGPVICOVEHPAVTGNLQTORYLEVQYKPOVHIQMTYPILOGLTR 240
DB 181 YTVTSQMLKVKHKEDDGPVICOVEHPAVTGNLQTORYLEVQYKPOVHIQMTYPILOGLTR 240
QY 241 EGDFAFELTCEAIGKPOQVMTWVRVDDENPOHVLSPNLFINNLTNDNGTYRCEASNI 300
DB 241 EGDFAFELTCEAIGKPOQVMTWVRVDDENPOHVLSPNLFINNLTNDNGTYRCEASNI 300
QY 301 VGKASDYMUYVDDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTSRAGEEGTIGAVDAVIG 360
DB 301 VGKASDYMUYVDDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTSRAGEEGTIGAVDAVIG 360
QY 361 GVAHVAVFAMLCIIILIGRYFAHKGTYFTHKAGDADADADATAIINAEGGONNSEKK 420
DB 361 GVAHVAVFAMLCIIILIGRYFAHKGTYFTHKAGDADADADATAIINAEGGONNSEKK 420
QY 421 EYF 423
DB 421 EYF 423

RESULT 2
US-09-778-187B-4
; Sequence 4, Application US/09778187B
; Patent No. US20020168712A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; TITLE OF INVENTION: MOLECULES DESIGNATED LDCAM
; FILE REFERENCE: 2873-US
; CURRENT APPLICATION NUMBER: US/09/778,187B
; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: PCT/US99/17905
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: US 60/095,672
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 423
; TYPE: PRT
; ORGANISM: mus musculus
US-09-778-187B-4

Query Match 100.0%; Score 2197; DB 9; Length 423;
Best Local Similarity 100.0%; Pred. No. 1.1e-170;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPGRLRLLLLSAAALIPTGDQNLFTKQVTVIEGVAATISCOVNSKSDSVIQLN 60
DB 1 AAPGRLRLLLLSAAALIPTGDQNLFTKQVTVIEGVAATISCOVNSKSDSVIQLN 60
QY 61 PNRQTIYFRDPRPKDSRFQNLNFSSELKVS/LTNVISDEGRYFCQLYTDPPOESYTTI 120
DB 61 PNRQTIYFRDPRPKDSRFQNLNFSSELKVS/LTNVISDEGRYFCQLYTDPPOESYTTI 120
QY 121 TVLVPRLNMLDIOKDTAVGEEIEVNCTAMASKPATIIRWFGKNKELKXKSEVEEWSM 180
DB 121 TVLVPRLNMLDIOKDTAVGEEIEVNCTAMASKPATIIRWFGKNKELKXKSEVEEWSM 180
QY 181 YTVTSQMLKVKHKEDDGPVICOVEHPAVTGNLQTORYLEVQYKPOVHIQMTYPILOGLTR 240
DB 181 YTVTSQMLKVKHKEDDGPVICOVEHPAVTGNLQTORYLEVQYKPOVHIQMTYPILOGLTR 240
QY 241 EGDFAFELTCEAIGKPOQVMTWVRVDDENPOHVLSPNLFINNLTNDNGTYRCEASNI 300
DB 241 EGDFAFELTCEAIGKPOQVMTWVRVDDENPOHVLSPNLFINNLTNDNGTYRCEASNI 300
QY 301 VGKASDYMUYVDDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTSRAGEEGTIGAVDAVIG 360
DB 301 VGKASDYMUYVDDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTSRAGEEGTIGAVDAVIG 360
QY 361 GVAHVAVFAMLCIIILIGRYFAHKGTYFTHKAGDADADADATAIINAEGGONNSEKK 420

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QY 421 EYF 423
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RESULT 3
US-10-302-041-22
; Sequence 22, Application US/10302041
; Publication No. US20030144478A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/10/302,041
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/778,510
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-302-041-22

Query Match 100.0%; Score 2197; DB 14; Length 423;
Best Local Similarity 100.0%; Pred. No. 1.1e-170;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPGRLRLLLLSAAALIPTGDQNLFTKQVTVIEGVAATISCOVNSKSDSVIQLN 60
DB 1 AAPGRLRLLLLSAAALIPTGDQNLFTKQVTVIEGVAATISCOVNSKSDSVIQLN 60
QY 61 PNRQTIYFRDPRPKDSRFQNLNFSSELKVS/LTNVISDEGRYFCQLYTDPPOESYTTI 120
DB 61 PNRQTIYFRDPRPKDSRFQNLNFSSELKVS/LTNVISDEGRYFCQLYTDPPOESYTTI 120
QY 121 TVLVPRLNMLDIOKDTAVGEEIEVNCTAMASKPATIIRWFGKNKELKXKSEVEEWSM 180
DB 121 TVLVPRLNMLDIOKDTAVGEEIEVNCTAMASKPATIIRWFGKNKELKXKSEVEEWSM 180
QY 181 YTVTSQMLKVKHKEDDGPVICOVEHPAVTGNLQTORYLEVQYKPOVHIQMTYPILOGLTR 240
DB 181 YTVTSQMLKVKHKEDDGPVICOVEHPAVTGNLQTORYLEVQYKPOVHIQMTYPILOGLTR 240
QY 241 EGDFAFELTCEAIGKPOQVMTWVRVDDENPOHVLSPNLFINNLTNDNGTYRCEASNI 300
DB 241 EGDFAFELTCEAIGKPOQVMTWVRVDDENPOHVLSPNLFINNLTNDNGTYRCEASNI 300
QY 301 VGKASDYMUYVDDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTSRAGEEGTIGAVDAVIG 360
DB 301 VGKASDYMUYVDDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTSRAGEEGTIGAVDAVIG 360
QY 361 GVAHVAVFAMLCIIILIGRYFAHKGTYFTHKAGDADADADATAIINAEGGONNSEKK 420
DB 361 GVAHVAVFAMLCIIILIGRYFAHKGTYFTHKAGDADADADATAIINAEGGONNSEKK 420
QY 421 EYF 423
DB 421 EYF 423

RESULT 4
US-10-015-115-112
; Sequence 112, Application US/10015115
; Publication No. US20030207800A1


```

; GENERAL INFORMATION:
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Zernusen, Bryan D
; APPLICANT: Paturajan, Meera
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesha
; APPLICANT: Gangoli, Esha A
; APPLICANT: Shinkets, Richard A
; APPLICANT: Taupier, Raymond J
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-211
; CURRENT APPLICATION NUMBER: US/10/015, 115
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/248,153
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 60/249,598
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/264,240
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/266,127
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/269,562
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/304,348
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/309,261
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/313,283
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 112
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-015-115-112

Query Match      100.0%; Score 2197; DB 15; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.1e-170;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      421 EYF 423
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DB      442 EYF 444

RESULT 5
US-10-015-115-113
; Sequence 113, Application US/10015115
; Publication No. US20030207800A1
; GENERAL INFORMATION:
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Zernusen, Bryan D
; APPLICANT: Paturajan, Meera
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesha
; APPLICANT: Gangoli, Esha A
; APPLICANT: Shinkets, Richard A
; APPLICANT: Taupier, Raymond J
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-211
; CURRENT APPLICATION NUMBER: US/10/015, 115
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/248,153
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 60/249,598
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/264,240
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/266,127
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/269,562
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/304,348
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/309,261
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/313,283
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 113
; LENGTH: 494
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-015-115-113

Query Match      99.1%; Score 2176.5; DB 15; Length 494;
Best Local Similarity 97.2%; Pred. No. 6.2e-169;
Matches 422; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

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D _b	360	VGRKSHSYMYLVYVDPRPTLPPTPTTTTTTTTTTTTTTTTTITDVTATPEPAVHDSRAEG	419
Q _y	350	TIGAVDAVYIGVVAWVFAMLCIIILGRYFAHKGITYFTHKAGDADADATAIINA	409
D _b	420	TIGAVDAVYIGVVAWVFAMLCIIILGRYFAHKGITYFTHKAGDADADATAIINA	479
Q _y	410	EGGQNNSEKKETP	423
D _b	480	EGGQNNSEKKETP	493

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RESULT 6
US-09-778-510-20
: Sequence 20 Application US/09778510
: Patent No. US20020164686A1
: GENERAL INFORMATION:
: APPLICANT: Baum, Peter
: TITLE OF INVENTION: Molecules Designated
: FILE REFERENCE: 2844-US
: CURRENT APPLICATION NUMBER: US/09/778, 510
: PRIOR FILING DATE: 2001-02-07
: PRIOR APPLICATION NUMBER: PCT/US99/17906
: PRIOR FILING DATE: 1999-08-05
: PRIOR APPLICATION NUMBER: 60/095,663
: PRIOR FILING DATE: 1998-08-07
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 20
: LENGTH: 442
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-778-510-20

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Query Match	98.7%	Score 2169	DB 9	Length 442
Best Local Similarity	98.8%	Pred. No. 2.2e-168		
Matches 418; Conservative	1	Mismatches 4	Indels 0	Gaps 0

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Db	19 AAPPGLRLIIILLSAALIPTGQGNLFTQDVVIEGEVAITISCOVNRKSDSVIQLN	78
QY	61 PNEQTIYFRDFRDLKDSRFQLNFSSSELSKSLNVISISDEGRYFCQLYTDPEQSYTTI	120
Db	79 PNEQTIYFRDFRDLKDSRFQLNFSSSELSKSLNVISISDEGRYFCQLYTDPEQSYTTI	138
QY	121 TVLVPRPNLMIDIQKOTAVEGEIEINCNMAASKATTIIRMFKNKELKKGSEVEEESDM	180
Db	139 TVLVPRPNLMIDIQKOTAVEGEIEINCNMAASKATTIIRMFKNKELKKGSEVEEESDM	198
QY	181 YTVTSQMLKVKHKEDGVPVICOVEHPATGNLQTRILEYQYKPOVHIQMTYPLQGLTR	240
Db	199 YTVTSQMLKVKHKEDGVPVICOVEHPATGNLQTRILEYQYKPOVHIQMTYPLQGLTR	258
QY	241 EGDALFELTCEAIKCPQVNVTVWRVDEKPCQHAVLSGNLFINNLKNTDNGTYCEASNT	300
Db	259 EGDALFELTCEAIKCPQVNVTVWRVDEKPCQHAVLSGNLFINNLKNTDNGTYCEASNT	318
QY	301 VGRASDYMLYVVDPEPTIIPRPTTTTTTTTTTTTTLIIINDRSAGEGTIGANDHAVIG	360
Db	319 VGRASDYMLYVVDPEPTIIPRPTTTTTTTTTTTTTLIIINDRSAGEGTIGANDHAVIG	378
QY	361 GVAAVVFVFMCLIIILGRYFARHKQYFTHEAKGADDAADATAIINAEQGNNSEKK	420
Db	379 GVAAVVFVFMCLIIILGRYFARHKQYFTHEAKGADDAADATAIINAEQGNNSEKK	438
QY	421 EYF 423	
Db	439 EYF 441	

```

1  RESULT 7
2  US-09-778-187B-2
3  ; Sequence 2, Application US/09778187B
4  ; Patent No. US0320168712A1
5  GENERAL INFORMATION:
6  APPLICANT: Baum, Peter R.
7  APPLICANT: Fenslow III, William C
8  TITLE OF INVENTION: MOLECULES DESIGNATED LDCAM
9  FILE REFERENCE: 2873-US
10 CURRENT APPLICATION NUMBER: US/09/778,187B
11 CURRENT FILING DATE: 2001-02-06
12 PRIOR APPLICATION NUMBER: PCT/US99/17905
13 PRIOR FILING DATE: 1999-08-05
14 PRIOR APPLICATION NUMBER: US 60/095,672
15 PRIOR FILING DATE: 1998-08-07
16 NUMBER OF SEQ ID NOS: 10
17 SOFTWARE: PatentIn version 3.1
18 SEQ ID NO: 2
19 LENGTH: 442
20 TYPE: prt
21 ORGANISM: homo sapiens
22 US-09-778-187B-2

```

Query Match	98.7%	Score 2169	DB 9	Length 442
Best Local Similarity	98.8%	Pred. No. 2.2e-168		
Matches 418; Conservative	1;	Mismatches 4;	Indels 0;	Gaps 0;

QY	AAAPGRLRLILLLLSAALI	PTGGQNLFTKDVI	EGEVAITISCVNKS	DDSVIQLLN	60	
Db	19	AAAPGRLRLILLLLSAALI	PTGGQNLFTKDVI	EGEVAITISCVNKS	DDSVIQLLN 78	
QY	61	PNRQTIYFDPRFLKDSRFQ	LLNFSSESELKVS	LNVSISDEGRYFCOLY	YDPDQESYTTI 120	
Db	79	PNRQTIYFDPRFLKDSRFQ	LLNFSSESELKVS	LNVSISDEGRYFCOLY	YDPDQESYTTI 138	
QY	121	TVLVPRLNIMIDIQD	TAVEGEIEVNCNMA	SKXATITIRPKNGKEL	KGSEVEEWSDM 180	
Db	139	TVLVPRLNIMIDIQD	TAVEGEIEVNCNMA	SKXATITIRPKNGKEL	KGSEVEEWSDM 198	
QY	181	YVTSOLMLKVHKEDD	GVVICOVHPAVTGNLQ	RTLEQYKPOVHIQMT	YPLQGLTR 240	
Db	199	YVTSOLMLKVHKEDD	GVVICOVHPAVTGNLQ	RTLEQYKPOVHIQMT	YPLQGLTR 258	
QY	241	EGAPFLTEBAIGKPO	PVMWTVVRYDDEN	POHAVISGNFLINLN	KTLNDGTTCESNI 300	
Db	259	EGAPFLTEBAIGKPO	PVMWTVVRYDDEN	POHAVISGNFLINLN	KTLNDGTTCESNI 318	
QY	301	VGRASHDNLVYVDP	PTTITPTTTTTTTTT	TTTTTTTTTTTTTTTT	TTTTTTTTTTTTTTTT 360	
Db	319	VGRASHDNLVYVDP	PTTITPTTTTTTTTT	TTTTTTTTTTTTTTTT	TTTTTTTTTTTTTTTT 378	
QY	361	GVVAVVVFMCLII	ILIGRFARAKQTY	FTHEAKGADDA	DADPTAIIINAE	GQNNSEKK 420
Db	379	GVVAVVVFMCLII	ILIGRFARAKQTY	FTHEAKGADDA	DADPTAIIINAE	GQNNSEKK 438
QY	421	EYF	423			
Db	439	EYF	441			

RESULT 8
 US-09-984-130-136
 : Sequence 136, Application US/09984130
 : Publication No. US20030055231A1
 : GENERAL INFORMATION:
 : APPLICANT: NI et al.
 : TITLE OF INVENTION: 12 Human Secreted Proteins
 : FILE REFERENCE: PF469P2
 : CURRENT APPLICATION NUMBER: US/09/984,130
 : CURRENT FILING DATE: 2001-10-29
 : PRIOR APPLICATION NUMBER: 60/243,792

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; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 09/836,353
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/198,407
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: PCT/US99/25031
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 60/105,971
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 136
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-836-130-136

Query Match      98.7%; Score 2169; DB 10; Length 442;
Best Local Similarity 98.8%; Pred. No. 2.2e-168;
Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPGRLRLILLLSAALIPITGQGNLFTKDVTVIEGEVATISQVKNKSDSVIQLLN 60
D 19 AAPGRLRLILLLSAALIPITGQGNLFTKDVTVIEGEVATISQVKNKSDSVIQLLN 78
QY 61 PNRQTIYFRDPRPLKDSRFQNLNFSSELKVSILNVSISDEGRYFCQLYTDPQESYTTI 120
D 79 PNRQTIYFRDPRPLKDSRFQNLNFSSELKVSILNVSISDEGRYFCQLYTDPQESYTTI 138
QY 121 TVLVPRLNMLDIOKDTAVEGEIEIVNCTAMASKPATIIRFWFKGNELKGSVEEWSMD 180
D 139 TVLVPRLNMLDIOKDTAVEGEIEIVNCTAMASKPATIIRFWFKGNELKGSVEEWSMD 198
QY 181 YTTVSQMLKVKHKEDDGVPIQVEHPAVTGNLQTORYLEVOYKQVHIQMTYPIQLTLR 240
D 199 YTTVSQMLKVKHKEDDGVPIQVEHPAVTGNLQTORYLEVOYKQVHIQMTYPIQLTLR 258
QY 241 EGDAPFELTCEALIGKQPVMTWVRVDEMPQHAVLSGPNLFNNLNKTNDGTYRCEASNI 300
D 259 EGDAPFELTCEALIGKQPVMTWVRVDEMPQHAVLSGPNLFNNLNKTNDGTYRCEASNI 318
QY 301 VGKASDYMLYVYDPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTSRAGEGIGAVDHA 360
D 319 VGKASDYMLYVYDPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTSRAGEGIGAVDHA 378
QY 361 GVAVVVFMCLLIIIGRYFARHKGYFTHEAKGADADADATAIINAEGQNNSEKK 420
D 379 GVAVVVFMCLLIIIGRYFARHKGYFTHEAKGADADADATAIINAEGQNNSEKK 438
QY 421 EYF 423
D 439 EYF 441

RESULT 9
US-09-836-353A-136
; Sequence 136, Application US/09836353A
; Publication No. US20030129685A1
; GENERAL INFORMATION:
; APPLICANT: NI et al.
; TITLE OF INVENTION: 12 Human Secreted Proteins
; FILE REFERENCE: PF489P1
; CURRENT APPLICATION NUMBER: US/09/836,353A
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/198,407
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: PCT/US99/25031
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 60/105,971
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 136
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; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-836-353A-136

Query Match      98.7%; Score 2169; DB 10; Length 442;
Best Local Similarity 98.8%; Pred. No. 2.2e-168;
Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPGRLRLILLLSAALIPITGQGNLFTKDVTVIEGEVATISQVKNKSDSVIQLLN 60
D 19 AAPGRLRLILLLSAALIPITGQGNLFTKDVTVIEGEVATISQVKNKSDSVIQLLN 78
QY 61 PNRQTIYFRDPRPLKDSRFQNLNFSSELKVSILNVSISDEGRYFCQLYTDPQESYTTI 120
D 79 PNRQTIYFRDPRPLKDSRFQNLNFSSELKVSILNVSISDEGRYFCQLYTDPQESYTTI 138
QY 121 TVLVPRLNMLDIOKDTAVEGEIEIVNCTAMASKPATIIRFWFKGNELKGSVEEWSMD 180
D 139 TVLVPRLNMLDIOKDTAVEGEIEIVNCTAMASKPATIIRFWFKGNELKGSVEEWSMD 198
QY 181 YTTVSQMLKVKHKEDDGVPIQVEHPAVTGNLQTORYLEVOYKQVHIQMTYPIQLTLR 240
D 199 YTTVSQMLKVKHKEDDGVPIQVEHPAVTGNLQTORYLEVOYKQVHIQMTYPIQLTLR 258
QY 241 EGDAPFELTCEALIGKQPVMTWVRVDEMPQHAVLSGPNLFNNLNKTNDGTYRCEASNI 300
D 259 EGDAPFELTCEALIGKQPVMTWVRVDEMPQHAVLSGPNLFNNLNKTNDGTYRCEASNI 318
QY 301 VGKASDYMLYVYDPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTSRAGEGIGAVDHA 360
D 319 VGKASDYMLYVYDPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTSRAGEGIGAVDHA 378
QY 361 GVAVVVFMCLLIIIGRYFARHKGYFTHEAKGADADADATAIINAEGQNNSEKK 420
D 379 GVAVVVFMCLLIIIGRYFARHKGYFTHEAKGADADADATAIINAEGQNNSEKK 438
QY 421 EYF 423
D 439 EYF 441

RESULT 10
US-10-363-616-262
; Sequence 262, Application US/10363616
; Publication No. US20040044181A1
; GENERAL INFORMATION:
; APPLICANT: HySeq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-113 (793)
; CURRENT APPLICATION NUMBER: US/10/363,616
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 09/654,935
; PRIOR FILING DATE: 2000-03-01
; NUMBER OF SEQ ID NOS: 490
; SEQ ID NO 262
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-616-262

Query Match      98.7%; Score 2169; DB 12; Length 442;
Best Local Similarity 98.8%; Pred. No. 2.2e-168;
Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPGRLRLILLLSAALIPITGQGNLFTKDVTVIEGEVATISQVKNKSDSVIQLLN 60
D 19 AAPGRLRLILLLSAALIPITGQGNLFTKDVTVIEGEVATISQVKNKSDSVIQLLN 78
QY 61 PNRQTIYFRDPRPLKDSRFQNLNFSSELKVSILNVSISDEGRYFCQLYTDPQESYTTI 120
D 79 PNRQTIYFRDPRPLKDSRFQNLNFSSELKVSILNVSISDEGRYFCQLYTDPQESYTTI 138
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QY 121 TVVPPRNLMIDIOKDTAVGEEIEVNCJAMASKPATTTIRFKGNELKXKSEVEEWSM 180
DB 139 TVVPPRNLMIDIOKDTAVGEEIEVNCJAMASKPATTTIRFKGNELKXKSEVEEWSM 198
QY 181 YTVTSQMLKVHKEDDGVPICOVEHPAVTGNLOTORYLEVQYKPOVHIOMTYPLQGLTR 240
DB 199 YTVTSQMLKVHKEDDGVPICOVEHPAVTGNLOTORYLEVQYKPOVHIOMTYPLQGLTR 258
QY 241 EGDALFELTCEAIGKPGQVMTWVRVDEMPQHAVLSGPNLFINNLTNGTYRCEASNI 300
DB 259 EGDALFELTCEAIGKPGQVMTWVRVDEMPQHAVLSGPNLFINNLTNGTYRCEASNI 318
QY 301 VGKASDYMXYVDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTSRAGEEGTIGAVDAVIG 360
DB 319 VGKASDYMXYVDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTSRAGEEGSIRAVDAVIG 378
QY 361 GVAVVVFPAMLCIIIIIGRYFAHKGTYFTHEAKGADDAADADATAIINAEAGGONNSEKK 420
DB 379 GVAVVVFPAMLCIIIIIGRYFAHKGTYFTHEAKGADDAADADATAIINAEAGGONNSEKK 438
QY 421 EYF 423
DB 439 EYF 441

RESULT 11

US-10-302-041-20
; Sequence 20, Application US/10302041
; Publication No. US20030144478A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/10/302, 041
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/778, 510
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095, 663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-302-041-20

Query Match 98.7%; Score 2169; DB 14; Length 442;
Best Local Similarity 98.8%; Pred. No. 2.2e-168;

Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPGLRLRLILLLLSAAALIPFGDGNLFTKDVYIEGEVATISCOVNSDSDSVIQLN 60
DB 19 AAPGLRLRLILLLLSAAALIPFGDGNLFTKDVYIEGEVATISCOVNSDSDSVIQLN 78
QY 61 PNRQTIYFRDPRPKDSRFQNLNFSSESELKVSILNVSISDEGRYFCOLYTDPPQESYTTI 120
DB 79 PNRQTIYFRDPRPKDSRFQNLNFSSESELKVSILNVSISDEGRYFCOLYTDPPQESYTTI 138
QY 121 TVVPPRNLMIDIOKDTAVGEEIEVNCJAMASKPATTTIRFKGNELKXKSEVEEWSM 180
DB 139 TVVPPRNLMIDIOKDTAVGEEIEVNCJAMASKPATTTIRFKGNELKXKSEVEEWSM 198
QY 181 YTVTSQMLKVHKEDDGVPICOVEHPAVTGNLOTORYLEVQYKPOVHIOMTYPLQGLTR 240
DB 199 YTVTSQMLKVHKEDDGVPICOVEHPAVTGNLOTORYLEVQYKPOVHIOMTYPLQGLTR 258
QY 241 EGDALFELTCEAIGKPGQVMTWVRVDEMPQHAVLSGPNLFINNLTNGTYRCEASNI 300
DB 259 EGDALFELTCEAIGKPGQVMTWVRVDEMPQHAVLSGPNLFINNLTNGTYRCEASNI 318

QY 301 VGKASDYMXYVDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTSRAGEEGTIGAVDAVIG 360
DB 319 VGKASDYMXYVDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTSRAGEEGSIRAVDAVIG 378
QY 361 GVAVVVFPAMLCIIIIIGRYFAHKGTYFTHEAKGADDAADADATAIINAEAGGONNSEKK 420
DB 379 GVAVVVFPAMLCIIIIIGRYFAHKGTYFTHEAKGADDAADADATAIINAEAGGONNSEKK 438
QY 421 EYF 423
DB 439 EYF 441

RESULT 12

US-10-403-107-1
; Sequence 1, Application US/10403107
; Publication No. US20030165974A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: REEVES, Roger
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS
; FILE REFERENCE: JHU1770-1
; CURRENT APPLICATION NUMBER: US/10/403,107
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US/09/930, 803
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-107-1

Query Match 98.7%; Score 2169; DB 14; Length 442;
Best Local Similarity 98.8%; Pred. No. 2.2e-168;
Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPGLRLRLILLLLSAAALIPFGDGNLFTKDVYIEGEVATISCOVNSDSDSVIQLN 60
DB 19 AAPGLRLRLILLLLSAAALIPFGDGNLFTKDVYIEGEVATISCOVNSDSDSVIQLN 78
QY 61 PNRQTIYFRDPRPKDSRFQNLNFSSESELKVSILNVSISDEGRYFCOLYTDPPQESYTTI 120
DB 79 PNRQTIYFRDPRPKDSRFQNLNFSSESELKVSILNVSISDEGRYFCOLYTDPPQESYTTI 138
QY 121 TVVPPRNLMIDIOKDTAVGEEIEVNCJAMASKPATTTIRFKGNELKXKSEVEEWSM 180
DB 139 TVVPPRNLMIDIOKDTAVGEEIEVNCJAMASKPATTTIRFKGNELKXKSEVEEWSM 198
QY 181 YTVTSQMLKVHKEDDGVPICOVEHPAVTGNLOTORYLEVQYKPOVHIOMTYPLQGLTR 240
DB 199 YTVTSQMLKVHKEDDGVPICOVEHPAVTGNLOTORYLEVQYKPOVHIOMTYPLQGLTR 258
QY 241 EGDALFELTCEAIGKPGQVMTWVRVDEMPQHAVLSGPNLFINNLTNGTYRCEASNI 300
DB 259 EGDALFELTCEAIGKPGQVMTWVRVDEMPQHAVLSGPNLFINNLTNGTYRCEASNI 318
QY 301 VGKASDYMXYVDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTSRAGEEGTIGAVDAVIG 360
DB 319 VGKASDYMXYVDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTSRAGEEGSIRAVDAVIG 378
QY 361 GVAVVVFPAMLCIIIIIGRYFAHKGTYFTHEAKGADDAADADATAIINAEAGGONNSEKK 420
DB 379 GVAVVVFPAMLCIIIIIGRYFAHKGTYFTHEAKGADDAADADATAIINAEAGGONNSEKK 438
QY 421 EYF 423
DB 439 EYF 441

RESULT 13

US-10-015-115-111
; Sequence 111, Application US/10015115
; Publication No. US20030207800A1
; GENERAL INFORMATION:
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Zernhusen, Bryan D
; APPLICANT: Patuturajan, Meera
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesha
; APPLICANT: Gangoli, Esna A
; APPLICANT: Shinkets, Richard A
; APPLICANT: Taupier, Raymond J
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCES: 21402-211
; CURRENT APPLICATION NUMBER: US/10/015,115
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/248,153
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 60/249,598
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/264,240
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/266,127
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/269,562
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/304,348
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/309,261
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/313,283
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 111
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-015-115-111
Query Match 98.7%; Score 2169; DB 15; Length 442;
Best Local Similarity 98.8%; Pred. No. 2.2e-168;
Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 AAPPGLRLRLILLISAAALIPFGDGNLFTKDVTVIEGVATTSCQVKKSDSVYQLLN 60
DB 19 AAPPGLRLRLILLISAAALIPFGDGNLFTKDVTVIEGVATTSCQVKKSDSVYQLLN 78
QY 61 PNRQTIYFRDFRPLKDSRFQNLNFSSELKVSILTNVSIISDEGRYFCQLYTDPPQESYTTI 120
DB 79 PNRQTIYFRDFRPLKDSRFQNLNFSSELKVSILTNVSIISDEGRYFCQLYTDPPQESYTTI 138
QY 121 TVLVPFRNLIMIDIOKDAVEGEIEVNCTAMASKPATIRFWKGNELKKGSEVEWSDM 180
DB 139 TVLVPFRNLIMIDIOKDAVEGEIEVNCTAMASKPATIRFWKGNELKKGSEVEWSDM 198
QY 181 YTVTSQMLKVKHKEDDGVPIQVEHPAVTGNLQTCRYLEVOYKPCQVHIQMTYPLQGLTR 240
DB 199 YTVTSQMLKVKHKEDDGVPIQVEHPAVTGNLQTCRYLEVOYKPCQVHIQMTYPLQGLTR 258
QY 241 EGDFAELITCEALIGFCQVMTWTVAVVDEMPQHAVLSGPNLFNNLNTDNGTRCEASNI 300
DB 259 EGDFAELITCEALIGFCQVMTWTVAVVDEMPQHAVLSGPNLFNNLNTDNGTRCEASNI 318
QY 301 VGKASDYMALVYDPTTIPPTTT 360
DB 319 VGKASDYMALVYDPTTIPPTTT 378

QY 361 GVAVAVFAMLCILLILGRYFARHKGTFTHEAKGADPADADPAIINAEGGQNNSEKK 420
DB 379 GVAVAVFAMLCILLILGRYFARHKGTFTHEAKGADPADADPAIINAEGGQNNSEKK 438
QY 421 EYF 423
DB 439 EYF 441
RESULT 14
US-10-015-115-110
; Sequence 110, Application US/10015115
; Publication No. US20030207800A1
; GENERAL INFORMATION:
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Zernhusen, Bryan D
; APPLICANT: Patuturajan, Meera
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesha
; APPLICANT: Gangoli, Esna A
; APPLICANT: Shinkets, Richard A
; APPLICANT: Taupier, Raymond J
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCES: 21402-211
; CURRENT APPLICATION NUMBER: US/10/015,115
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/248,153
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 60/249,598
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/264,240
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/266,127
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/269,562
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/304,348
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/309,261
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/313,283
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 110
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-015-115-110
Query Match 98.6%; Score 2166; DB 15; Length 442;
Best Local Similarity 98.6%; Pred. No. 3.9e-168;
Matches 417; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 AAPPGLRLRLILLISAAALIPFGDGNLFTKDVTVIEGVATTSCQVKKSDSVYQLLN 60
DB 19 AAPPGLRLRLILLISAAALIPFGDGNLFTKDVTVIEGVATTSCQVKKSDSVYQLLN 78
QY 61 PNRQTIYFRDFRPLKDSRFQNLNFSSELKVSILTNVSIISDEGRYFCQLYTDPPQESYTTI 120
DB 79 PNRQTIYFRDFRPLKDSRFQNLNFSSELKVSILTNVSIISDEGRYFCQLYTDPPQESYTTI 138
QY 121 TVLVPFRNLIMIDIOKDAVEGEIEVNCTAMASKPATIRFWKGNELKKGSEVEWSDM 180
DB 139 TVLVPFRNLIMIDIOKDAVEGEIEVNCTAMASKPATIRFWKGNELKKGSEVEWSDM 198
QY 181 YTVTSQMLKVKHKEDDGVPIQVEHPAVTGNLQTCRYLEVOYKPCQVHIQMTYPLQGLTR 240

Db 199 YTVTSQMLKVKHEDDGVPIQVEHPAVTGNLTQRYLEVQYKPGVHIQMTYPLQGLTR 258
QY 241 EGDAPFLTCEAIGKPGPVMTWVRVDDMPQHAVLGSEPNLFINNLKNTDNGTYRCEASNI 300
Db 259 EGDALLETCEAIGKPGPVMTWVRVDDMPQHAVLGSEPNLFINNLKNTDNGTYRCEASNI 318
QY 301 VGKASDYMVLVYDPPPTTITTT 360
Db 319 VGKASDYMVLVYDPPPTTITTT 378
QY 361 GVAVVVVFAMLCIIIIIGRYFARHKGTYFTHAKGADDAADADTAIINAEQGNNSSEKK 420
Db 379 GVAVVVVFAMLCIIIIIGRYFARHKGTYFTHAKGADDAADADTAIINAEQGNNSSEKK 438
QY 421 EYF 423
Db 439 EYF 441

RESULT 15

US-09-866-028-61
; Sequence 61, Application US/09866028
; Patent No. US20020058309A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerlitsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavich, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PAM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-866-028-61

Query Match 97.8%; Score 2149; DB 9; Length 440;

Best Local Similarity 98.3%; Pred. No. 9.3e-167;
Matches 416; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

QY 1 AAPPGLRLRLILLLLSAALIPTGDQNLFTKDYTVIEGEVATISQVKNKSDSDSVTQLIN 60
Db 19 AAPPG--LRLLLLFSAALIPTGDQNLFTKDYTVIEGEVATISQVKNKSDSDSVTQLIN 76
QY 61 PNRQTIYFRDFRPLKDSRFQLNFSSESEKVSITNVSISDEGRYFCQLYTDPPQESYTTI 120
Db 77 PNRQTIYFRDFRPLKDSRFQLNFSSESEKVSITNVSISDEGRYFCQLYTDPPQESYTTI 136
QY 121 TVLVPPRNLMIDIQKOTAVGEEIEVNTAMASKPAATTIRWFKGNKELKGKSEVEBWSDM 180
Db 137 TVLVPPRNLMIDIQKOTAVGEEIEVNTAMASKPAATTIRWFKGNTELKGKSEVEBWSDM 196
QY 181 YTVTSQMLKVKHEDDGVPIQVEHPAVTGNLTQRYLEVQYKPGVHIQMTYPLQGLTR 240
Db 197 YTVTSQMLKVKHEDDGVPIQVEHPAVTGNLTQRYLEVQYKPGVHIQMTYPLQGLTR 256

QY 241 EGDAPFLTCEAIGKPGPVMTWVRVDDMPQHAVLGSEPNLFINNLKNTDNGTYRCEASNI 300
Db 259 EGDALLETCEAIGKPGPVMTWVRVDDMPQHAVLGSEPNLFINNLKNTDNGTYRCEASNI 316
QY 301 VGKASDYMVLVYDPPPTTITTT 360
Db 319 VGKASDYMVLVYDPPPTTITTT 376
QY 361 GVAVVVVFAMLCIIIIIGRYFARHKGTYFTHAKGADDAADADTAIINAEQGNNSSEKK 420
Db 379 GVAVVVVFAMLCIIIIIGRYFARHKGTYFTHAKGADDAADADTAIINAEQGNNSSEKK 436
QY 421 EYF 423
Db 439 EYF 439

Search completed: July 7, 2004, 06:39:09
Job time : 607.382 secs

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